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(54) Title: COMPOSITIONS AND METHODS FOR TREATING COAGULATION RELATED DISORDERS

(57) Abstract: Disclosed are methods for preventing or treating sepsis, a sepsis-related condition or an inflammatory disease in
a mammal. In one embodiment, the method includes administering to the mammal a therapeutically effective amount of at least
one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to tissue factor (TF) to form a complex in
which factor X or factor IX binding to the complex is inhibited and the administration is sufficient to prevent or treat the sepsis in
the mammal. The invention has a wide spectrum of useful applications including treating sepsis, disorders related to sepsis, and
inflammatory diseases such as arthritis.

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**COMPOSITIONS AND METHODS FOR TREATING
COAGULATION RELATED DISORDERS**

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10 **FIELD OF THE INVENTION**

The present invention features compositions and methods for preventing or
treating disorders that relate to undesired activation of blood coagulation. In some
instances, the coagulation contributes to certain inflammatory diseases and related
disorders. In one aspect, the invention provides methods for treating such disorders
15 by administering a therapeutically effective amount of a chimeric or humanized
antibody that binds tissue factor (TF) specifically. The invention has a wide spectrum
of important applications including use in the prevention or treatment of
inflammation including sepsis and arthritis.

20 **BACKGROUND OF THE INVENTION**

There is increasing recognition of relationship between coagulation and
inflammation. For instance, certain coagulation factors are thought to activate pro-
inflammatory cells and elicit inflammatory responses. On the other hand, some pro-
inflammatory cytokines have been reported to induce TF expression and generate
25 coagulation factors. Studies in certain primates support existence of the relationship
by showing that certain anticoagulants reduce inflammation. See F. B. Taylor Jr. *et
al., J. Clin. Invest.* **79**:918-925 (1987); M. Levi *et al., J. Clin. Invest.* **93**:114-120
(1994); and M. C. Minnema *et al., Blood* **95**:1117-23 (2000).

30   Much has been reported about blood coagulation. For instance, thrombin is a
blood protein that is believed to provide a link between coagulation and
inflammation. Most thrombin is generated by TF-initiation of the coagulation
cascade. Other key coagulation factors include Factor VIIa and Factor Xa.

Thrombin is thought to occupy multiple roles in pro-coagulant, anticoagulant, inflammatory, and mitogenic responses. See generally L. Styer, *Biochemistry*, 3rd Ed., W.H. Freeman Co., New York; and A.G. Gilman *et al.*, in *The Pharmacological Basis of Therapeutics*, 8th Ed., McGraw-Hill Inc., New York.

5

Certain infectious agents are thought to disturb the TF-initiated coagulation cascade. Fortunately, localized activation of the coagulation cascade often keeps the disturbance in check. Sometimes however, aberrant TF expression leads to serious and potentially life-threatening thrombotic disorders. For example, it has been

10   suggested that bacterial induction of TF expression can lead to sepsis, disseminated intravascular coagulation (DIC), widespread fibrin deposition, and other complications. The increase in TF expression is thought to be an important factor in facilitating progression of these disorders. An example of progression of an inflammatory disorder is the progression of acute lung injury (ALI) to acute

15   respiratory distress syndrome (ARDS) followed by progressive injury involving additional organ systems, such as the kidneys, leading to progressively more severe forms of sepsis. See Welty-Wolf, K. *et al. Am. J. Respir. Crit. Care Med.* **164**:1988 (2001), for instance.

20   There have been attempts to understand coagulation related disorders such as sepsis.

For instance, sepsis is a term that has used to characterize a spectrum of clinical conditions facilitated by a host immune response to infection, trauma, or

25   both. Sepsis has been characterized as an uncontrolled cascade of blood coagulation, fibrinolysis, and inflammation. At certain steps in the cascade, an auto-amplification process contributes to an acceleration of coagulation abnormalities, undesired inflammation, and endothelial injury. The amplification process is the result of inflammatory cytokines up-regulating the expression of TF on cells such as

30   endothelial cells and monocytes, resulting in increased activation of the coagulation cascade, which in turn results in the activation of PAR receptors and the up-

regulation of the production of inflammatory cytokines. See Osterud, B. *et al.*, *Thromobsis Hemost.* **83**:861 (2000); Mechtcheriakova, D. *et al.*, *FASEB J.* **15**:230 (2001); Shen, B.-Q. *et al.*, *J. Biol. Chem.* **276**:5281 (2001).

5   More specifically, sepsis has been characterized by systemic activation of inflammation and blood coagulation. Fibrinolyisis can be suppressed. Some research has pointed to a hemostatic imbalance that is thought to promote e.g., DIC and microvascular thrombosis. These and related indication are believed to impact normal organ function which can lead to death.

10

Sepsis and related disorders continue to be linked to patient contact with hospitals and out-patient clinics. Accordingly, managing these disorders is a prime concern of many health administrators, clinicians and insurers.

15   There are reports that undesired activation of blood coagulation is a key feature of certain inflammatory diseases. For example, extravascular fibrin deposition has been found in the autoimmune lesions of patients with rheumatoid arthritis (RA), glomerulonephritis, multiple sclerosis, psoriasis, Sjogren's syndrome and inflammatory bowel disease. See Weinberg, *et al.*, *Arthritis Rheum.* **34**:996-1005

20   (1991); Wakefield, *et al.*, *J Clin Pathol* **47**:129-133 (1994); Schoph, *et al.*, *Arch Dermatol Res* **285**:305-309 (1993); Zeher, *et al.*, *Clin Immunol Immunopathol* **71**:149-155 (1994); More, *et al.*, *J Clin Pathol* **46**:703-708 (1993).

Moreover, elevated TF levels are thought to be associated with systemic lupus

25   erythematosus. See Segal, *et al.*, *J Rheumatol* **27**:2827-2832 (2000). See also Nakano, *et al.*, *Clin Exp Rheumatol* **17**:161-170 (1999); Morris, *et al.*, *Ann Rheum Dis* **53**:72-79 (1994); Furmaniak-Kazmierczak, *et al.*, *J Clin Invest* **94**:472-480 (1994); Bokarewa, *et al.*, *Inflamm Res* **51**:471-477 (2002).

30   There have been suggestions that certain inflammatory conditions may be treated by blocking thrombosis. See R. Gordon *et al.*, *The New England Journal of*

Medicine **344**:699-709, 759-762 (2001). Certain anti-TF antibodies have been reported to be of some help in reducing some types of inflammation. See Levi, M. *et al.*, *supra.*

5   There have been efforts to develop antibodies that bind blood coagulation factors.

           For instance, U.S. Pat. Nos. 5,986,065 and 6,555,319 to Wong, H. *et al.* and PCT/US98/04644 (WO 98/40408) disclose a variety of such antibodies. Specifically

10   provided are murine antibodies, chimeric antibody derivatives and fragments thereof with significant binding affinity and specificity for tissue factor (TF). Use of chimeric antigen binding molecules are believed to reduce risk of an undesired immune response in human patients. See also S. L.Morrison and V. Oi, *Adv. Immunol.* **44**:65 (1989) (reporting methods of making human-mouse chimeric

15   antibodies).

           A variety of approaches have been used to make antibodies more immunologically acceptable to humans. Some use recombinant DNA technologies. For instance, one strategy has been to clone and modify non-human antibodies to

20   more closely resemble human antibodies. Collectively, such antibodies have been referred to as "humanized". See U.S Pat. Nos. 5,766,886 to Studnicka *et al.*; 5,693,762 to Queen *et al.*; 5,985,279 to Waldeman *et al.*; 5,225,539 to Winter; 5,639,641 to Pedersen, *et al.*; and references cited therein for methods of making and using humanized antibodies.

25

           Additional strategies for making humanized antibodies have been reported. See E. Padlan *Mol. Immunol.* **28**:489 (1991); Jones *et al.*, *Nature* **321**:522-525 (1986); Junghans *et al.*, *supra*; and Roguska, *et al.*, *PNAS (USA)* **91**:969 (1994). See also published U.S Patent Applications 2003/0109860 A1 and 2003/0082636.

30

It is unclear if prior antibodies are robust enough to block or reduce undesired activation of blood coagulation. More specifically, it is unclear if such antibodies are potent enough to prevent or treat sepsis and inflammatory diseases such as arthritis.

5   **SUMMARY OF THE INVENTION**

The present invention features compositions and methods for preventing or treating disorders relating to undesired activation of blood coagulation. In one aspect, the invention provides methods for preventing or treating such disorders by administering to a mammal a therapeutically effective amount of a chimeric or

10   humanized antibody that binds tissue factor (TF). The invention has a wide spectrum of important applications including use in the treatment of sepsis and inflammatory diseases such as arthritis.

We have found that antibodies and antigen binding fragments thereof that

15   specifically bind an epitope predominant to native human TF are suitable for preventing or treating disorders relating to undesired activation of blood coagulation. Preferred antibodies and fragments specifically bind native human TF and do not substantially bind non-native or denatured TF. More particular antibodies and fragments suitable for use with the present invention bind human TF so that at least

20   one of Factor X (FX) and Factor IX (FIX) do not effectively bind to the TF-Factor VIIa complex. Additionally preferred antibodies and fragments reduce or block TF function, typically by reducing or blocking FX binding or gaining access to TF molecules. Further preferred antibodies and fragments suitable for use with the invention do not significantly inhibit or block interaction or binding between TF and

25   Factor VIIa, or inhibit or block activity of a TF-Factor VIIa complex with respect to materials other than FX or FIX.

As discussed, it is believed that undesired activation of blood coagulation underlies sepsis and a variety of specific inflammatory diseases. More specifically,

30   unwanted TF-mediated coagulation is thought to initiate and/or prolong such disorders in many cases. It is thus an object of the present invention to provide

antibodies and fragments thereof that specifically bind TF to reduce or inactivate many if not all TF-associated functions. Such functions include, but are not limited to, blocking or inhibiting at least one of FIX and FX binding to the TF complex. Without wishing to be bound to theory, it is believed that by blocking or inhibiting

5   binding of at least one of those factors to the TF complex, activation of unwanted blood coagulation can be reduced or in some cases eliminated. That is, by blocking or inhibiting such unwanted processes according to the invention, it is believed that it is possible to prevent, treat or alleviate symptoms associated with sepsis and specific inflammatory diseases.

10

Preferably, such antibodies and fragments thereof are chimeric or humanized and are generally suitable for use in primates and particularly human patients in need of treatment.

15   There is recognition that sepsis and related conditions result from a potent and potentially life-threatening immune response to infection, trauma, or both. Typically, blood throughout the vasculature is subject to coagulation, resulting in complications such as inflammation, disseminated intravascular coagulation (DIC), clotting, and organ distress. Death can ensue in a matter of hours or less unless the condition is

20   treated rapidly. Prior to the present invention, it was not clear if any anti-TF antibody or TF-binding fragment would be robust enough to prevent or treat sepsis and related conditions.

However, it has been found that the anti-TF binding antibodies described herein are robust enough (*i.e.*, bind human TF specifically enough and with

25   appropriate avidity) to inhibit or block unwanted activation of the coagulation cascade. It has also been found that such activity is beneficial and can be used to prevent or treat sepsis and related conditions. As discussed below, we have found that such antibodies and fragments show good attenuation of inflammation,

30   disseminated intravascular coagulation (DIC), clotting, organ distress and related conditions in an *in vivo* animal model of human sepsis.

Such potent blocking or inhibition of the blood coagulation cascade has also been found to be highly useful in the prevention or treatment of certain inflammatory diseases. Without wishing to be bound to theory, it is believed that by using the

5   invention to block or reduce undesired activation of blood coagulation, it is possible to prevent, treat or alleviate symptoms associated with one or a combination of the inflammatory diseases. Importantly, the anti-TF binding antibodies described herein have been found to be robust enough to inhibit or block unwanted activation of the coagulation cascade, thereby helping to prevent, treat or alleviate symptoms

10 associated with arthritis and other inflammatory diseases.

Accordingly, and in one aspect, the invention provides a method for preventing or treating at least one of sepsis and an inflammatory disease in a mammal. In one embodiment, the method includes administering to the mammal a

15 therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to human TF to form a complex. A more preferred antibody reduces or blocks at least one of FX and FIX binding to the complex. Practice of the method is highly useful for preventing, treating, or reducing the severity of symptoms associated with sepsis and inflammatory diseases

20 including, but not limited to, rheumatoid arthritis (RA).

The present invention provides other important uses and advantages.

For instance, we have discovered that preferred humanized antibodies,

25 chimeric antibodies and fragments thereof desirably block at least one of FX and FIX binding to the TF-FVIIa complex. Preferably, such antibodies and fragments also inhibit or block FX or FIX activation by the complex. Surprisingly, such antibodies, when tested in the *in vivo* animal of human sepsis provided herein, are robust enough to prevent, treat or alleviate symptoms of sepsis and related complications. Also

30 surprisingly, such preferred antibodies and fragments are robust enough to prevent, treat, or alleviate symptoms associated with particular inflammatory diseases.

7

Importantly, preferred use of the present invention has identified and takes advantage of a particular immunological target (epitope) on the human TF molecule that can be exploited to prevent, treat, or alleviate symptoms associated with these indications.

5   The invention is flexible and can be used in a variety of settings in which sepsis and inflammatory diseases may be suspected or predominate.

For instance, and in one embodiment, the invention can be used in hospitals, clinics and other medical settings where sepsis has become a major health problem.

10   Especially problematic has been emergence of antibiotic resistance microorganisms such as bacteria which, if present in the blood, can rapidly produce septic shock and related complications. Practice of the invention can be used to hold the sepsis or related condition at bay while caregivers identify an appropriate treatment protocol, or perhaps reverse the effects of sepsis. It is thus anticipated as an object of the

15   invention to provide sepsis prevention or treatment methods in which administration of the antibodies and fragments disclosed herein may be combined with administration of one or more antibiotics.

The invention finds further use in emergency medical settings (*e.g.*,

20   ambulance, combat) in which the prevention and treatment methods disclosed herein can be administered at the point of care. Thus in one invention embodiment, the sepsis or sepsis-related condition can be held under some control while the patient is transported to a hospital or clinic for evaluation and treatment.

25   In other invention embodiments, the invention can be used to prevent, treat or reduce symptoms associated with arthritis and especially rheumatoid arthritis. For instance, by blocking or reducing the unwanted activation of blood coagulation, it is now possible to reduce the painful inflammation, pathological tissue destruction and remodeling typically associated with arthritis and related inflammatory diseases.

30

In another aspect, the invention provides a kit for performing the methods of this invention. In one embodiment, the kit includes at least one humanized antibody, chimeric antibody, or fragment thereof provided herein.

5   The invention also provides a method for reducing cytokine production in a mammal. In one embodiment, the method includes administering to the mammal a therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to tissue factor (TF) to form a complex. Preferably, Factor X or Factor IX binding to the complex is inhibited and

10   the administration is sufficient to reduce the cytokine production in the mammal. Suitable humanized antibodies, chimeric antibodies and fragments thereof are disclosed above and in the discussion and examples that follow.

Further provided by the present invention is a method for preventing or

15   treating a sepsis-related condition in a mammal. In one embodiment, the method includes administering to the mammal a therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to tissue factor (TF) to form a complex. Preferred antibodies and fragments are described herein and include those in which Factor X or factor IX

20   binding to the complex is inhibited. Preferably, administration is sufficient to prevent or treat the condition in the mammal.

The invention further provides a method for preventing or treating sepsis-induced anemia in a mammal. In one embodiment, the method includes

25   administering to the mammal a therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to tissue factor (TF) to form a complex. Preferred antibodies and fragments are disclosed herein including those in which Factor X or Factor IX binding to the complex is inhibited. Preferably, the administration is sufficient to prevent or treat

30   the condition in the mammal.

Other aspects of the invention are discussed *infra*.

BRIEF DESCRIPTION OF THE DRAWINGS

Figs. 1A and 1B shows the nucleic acid (SEQ ID NOS: 1 and 3) and amino

5   acid (SEQ ID NOS: 2 and 4) sequences of light chain and heavy chain variable

domains of H36.D2.B7, the murine anti-tissue factor antibody, with hypervariable

regions (CDRs or Complementarity Determining Regions) underlined (single

underline for nucleic acid sequences and double underline for amino acid sequences).

10   Fig. 2 is a drawing showing a plasmid map of humanized anti-TF IgG1

antibody expression vector (pSUN-34).

Figs. 3A-D are sequences of partially and fully humanized light chain (LC)

variable domains of the anti-TF antibody (SEQ ID NO.: ____). Fig. 3A shows the

15   sequence named "LC-09" which is representative of a fully humanized LC

framework (SEQ ID NO.:____). Light chain CDR sequences of cH36 and LC-09 are

shown in Figs. 3B-D (SEQ ID NOS.: _____, respectively).

Figs. 4A-D are drawings showing the sequences of partially and fully

20   humanized heavy chain (HC) variable domains of the anti-TF antibody (SEQ ID

NOS.: _____). Fig. 4A shows the sequence named "HC-08" which is representative

of a fully humanized HC framework (SEQ ID NO.:____). Heavy chain CDR

sequences for cH36 and HC-08 are shown in Figs. 4B-D (SEQ ID NOS.: _____,

respectively).

25

Figs. 5A-B are sequences showing human constant domains in the IgG1 anti-

tissue factor antibody (hOAT), with Fig. 5A showing the human kappa light chain

constant domain (SEQ ID NO.: ____) and Fig. 5B showing the human IgG1 heavy

chain constant domain (SEQ ID NO.: ___). The figures show hOAT (IgG1) constant

30   domain amino acid sequences.

Figs. 6A-B are sequences showing human constant domains in the IgG4 anti-tissue factor antibody (hFAT) with Fig. 6A showing the human kappa light chain constant domain (SEQ ID NO.: ____) and Fig. 6B showing the human IgG4 heavy chain constant domain (SEQ ID NO.: _____).

5

Figs. 7A-D are graphs showing a change in plasma IL-6 and IL-8 (Figs. 7A-B) concentrations (Figs. 7A-B); or IL-1β and TNF-α concentrations (Figs. 7C-D) in rhesus monkeys following an infusion of live *E.coli* in a lethal sepsis model.

10

Figs. 8A-C are graphs showing that cH36 attentuates sepsis-induced acute lung injury (ALI). In the figures, $AaDO_2$ is in mmHg, time in hours, pulmonary system compliance (Cst) in ml/cm water, and pulmonary arterial pressure (PAM) in mmHg.

15

Figures. 9A-B are graphs showing Kidney Myeloperoxidase (A) and Small Bowel Wet/Dry Weight Ratio (B) in Baboons.

Figure 10A-D are graphs showing that cH36 attenuates sepsis and related conditions in baboons. cH36 attenuates sepsis-induced coagulopathy (fibrinogen in 20 mg/DL; time in hours; partial prothrombin time (PTT) in seconds; and TAT in micrograms/L).

Figures 11A-B are graphs showing that elevations in serum IL-8 (A) and IL-6(B) are attenuated by treatment with cH36.

25

Figure 12 is a graph showing that elevations in bronchial alveolar levage IL-8, IL-6 and TNFR1 levels attenuated by treatment with cH36.

Figures 13A-C are graphs showing mean urine output (13A), mean blood pH 30 (13B), and serum bicarbonate levels (13C) in baboons treated with control and cH36 antibodies.

DETAILED DESCRIPTION OF THE INVENTION

As discussed, the invention provides a method for preventing, treating, or alleviating symptoms associated with sepsis or inflammatory diseases such as

5   arthritis. Practice of the method involves administering to a mammal in need of such treatment a therapeutically effective amount of at least one of a humanized antibody, chimeric antibody, or human TF-binding fragment to prevent or treat these diseases and related conditions.

10   There have been efforts to understand the etiology of sepsis and conditions related to sepsis. For instance, there is recognition that early events in the sepsis cascade are triggered by the host's immune response, thereby facilitating damaging actions on the vascular endothelium. Subendothelial structures are exposed and collagenases are liberated. Endothelial cells expressing tissue factor (TF) are

15   exposed, triggering the extrinsic pathway for activation of the coagulation cascade and accelerating the production of thrombin. Concurrently, the endothelial damage causes further exacerbation of inflammation, resulting in neutrophil activation, neutrophil-endothelial cell adhesion, and further elaboration of inflammatory cytokines. These inflammatory processes further contribute to vascular endothelial

20   dysfunction. Endogenous modulators of homeostasis, such as protein C and anti-thrombin III (AT III), are consumed and their levels become deficient as the body attempts to return to a normal functional state. Under normal conditions, the endothelial surface proteins thrombomodulin and endothelial protein C receptor (EPCR), activate protein C and its modulating effects. In sepsis, the endothelial

25   damage impairs this function of thrombomodulin and EPCR, thereby contributing to the loss of control. Left unopposed, the endothelial damage accumulates. This uncontrolled cascade of inflammation and coagulation fuels the progression of sepsis, resulting in hypoxia, widespread ischemia, organ dysfunction, and ultimately death for a large number of patients.

30

By the phrase "sepsis-related condition" is meant those known to precede, accompany, or follow sepsis including, but not limited to, disseminated intravascular coagulation (DIC), fibrin deposition, thrombosis, and lung injury, including acute lung injury (ALI), or acute respiratory distress syndrome (ARDS). A particular type

5   of lung injury amenable to prevention or treatment by use of the invention is sepsis-induced acute lung injury. See Welty-Wolf, *et al., Am. J. Respir. Crit. Care Med.* **164**:1988 (2001), for instance. Also encompassed are certain renal disorders accompanying sepsis such as acute tubular necrosis (ACN) and related conditions.

10   Acute lung injury (ALI) and acute respiratory distress syndrome (ARDS) are severe disorders that continue to receive significant attention. In particular, an important feature of ALI and ARDS, is local activation of extrinsic coagulation and inhibition of fibrinolysis. As the injury evolves, these perturbations have been reported to cause deposition of fibrin in the microvascular, interstitial, and alveolar

15   spaces of the lung leading to capillary obliteration and hyaline membrane formation. Components of the extrinsic coagulation pathway (*e.g.* tissue factor (TF), thrombin, and fibrin) signal alterations in inflammatory cell traffic and increases in vascular permeability. Procoagulants and fibrin are also thought to promote other key events in the injury including complement activation, production of pro-inflammatory

20   cytokines, inhibition of fibrinolysis, and remodeling of the injured lung. Without wishing to be bound to theory, it is believed that by reducing or blocking these initiating events (extrinsic coagulation) and downstream effects (pro-inflammatory events) in the lungs, disordered fibrin turnover can be reduced or blocked and the evolution of severe structural and functional injury can be reduced or averted during

25   ALI/ARDS. Coagulation blockade can target the TF-Factor VIIa (TF-FVIIa) complex at several points, but the effects of these different strategies on inflammation and the development of lung injury are still being confirmed. The Examples show use of a chimerized monoclonal antibody against human TF (cH36) and its Fab fragment (cH36-Fab) in blocking initiation of coagulation in gram-negative sepsis

30   and prevent acute lung injury.

The present invention is intended, in one embodiment, to prevent or treat sepsis and sepsis related conditions (such as DIC, ALI and ARDS) by reducing or blocking activity of a key component of the blood coagulation cascade (*i.e.*, TF). Preferred humanized antibodies, chimeric antibodies, and fragments thereof

5   specifically bind human TF typically to block at least one of FX or Factor IX binding to the TF complex. Typically, such preferred antibodies and fragments also inhibit or block FX or FIX activation of that complex. Thus, the compositions and methods of the invention reduce or block unwanted activation of the blood coagulation cascade by decreasing or preventing activity of a key molecular component.

10

Such preferred antibodies are different from prior antibodies such as those provided by U.S. Pat. No. 6,274,142 ("'142") to O'Brien et al. For instance, the '142 patent reports TF neutralizing antibodies that cannot bind to Factor VII/VIIa or effect proteolysis of Factors IX or X. In contrast, preferred antibodies of the invention

15   substantially reduce or block at least one of FX or FIX binding to the TF complex. See also PCT/US01/07501 (WO 01/70984).

As mentioned previously, unwanted coagulation activation is a prominent feature of certain inflammatory diseases, particularly those associated with

20   autoimmunity. See Weinberg, *et al.*, *Arthritis Rheum.* 34:996-1005 (1991); Kincaid-Smith, *Kidney Int* 7:242-253 (1975); Wakefield, *et al.*, *J Clin Pathol* 47:129-133 (1994); Schoph, *et al.*, *Arch Dermatol Res* 285:305-309 (1993); Zeher, *et al.*, *Clin Immunol Immunopathol* 71:149-155 (1994); More, *et al.*, *J Clin Pathol* 46:703-708 (1993). Elevated TF levels have been reported to be associated with disease activity

25   in systemic lupus erythematosus. See Segal, *et al.*, *J Rheumatol* 27:2827-2832 (2000). It is thus an object of this invention to help control tissue factor-mediated coagulation, thereby reducing or in some instances blocking the inflammation, pathological tissue destruction and undesired remodeling that is a hallmark of many inflammatory diseases.

30

By the phrase "inflammatory disease" including plural forms is meant a pathological condition associated with an unwanted TF-mediated activation of the coagulation. Preferred inflammatory diseases are usually associated with a known or suspected autoimmune condition. Typically, such diseases are further associated with

5   enhanced production of pro-inflammatory cytokines and/or chemokines as determined by standard methods. Examples of such cytokines include IL-1, TNFα, GM-CSF, M-CSF, IL-6, LIF, IL-15, IFNα, and IL12. Examples of such chemokines include IL-8, MIP-1α, MIP-1β, MCP-1, ENA-78, and RANTES. Typically, but not exclusively, one or more of neovascularization and extravascular fibrin deposition is

10   associated with the inflammatory disease. More particular examples of inflammatory diseases according to the invention include arthritis, preferably rheumatoid arthritis (RA); glomerulonephritis, multiple sclerosis, psoriasis, Sjogren's syndrome and inflammatory bowel disease. Arthritis can be readily detected by one or a combination of features including presence of synovial inflammation, pannus

15   formation, and cartilage destruction.

Preferred use of the invention will help reduce, prevent or alleviate symptoms of the inflammatory disease typically by decreasing TF-mediated coagulation activation. Such activation by TF is believed to provide many disadvantages

20   including, but not limited to, supporting the production of inflammatory molecules, enhancing proinflammatory cell activity, increasing tissue destruction, increasing unwanted remodeling and boosting angiogenesis. The invention thus provides a new and fundamental means for addressing inflammatory disease by providing compositions and methods for specifically binding and inhibiting function of TF.

25

Practice of the invention will particularly help in the prevention and treatment of inflammatory autoimmune diseases. Recent work is in agreement with this inventive concept. See Marty, *et al.*, *J Clin Invest* **107**:631-640 (2001); Varisco, *et al.*, *Ann Rheum Dis* **59**:781-787 (2000); Busso, *et al.*, *Arthritis Rheum* **48**:651-659

30   (2003).

As discussed, the U.S. Pat. Nos. 5,986,065 and 6,555,319 to Wong, H. *et al.* and PCT/US98/04644 (WO 98/40408) disclose a variety of murine anti-TF antibodies and antigen binding fragments with good human TF binding characteristics. Such

5   antibodies and fragments can be employed in accord with the present invention. Additionally, such antibodies and fragments can be used to treat experimentally induced sepsis, for instance, in a relevant rodent model. However, and as will be appreciated, such murine antibodies and fragments are not usually appropriate for use in other mammals such as primates and especially human subjects. Further suitable

10   antibodies and fragments are disclosed by U.S. Patent Application Publication No. 20030082636; WO 03/037911 and WO 98/40408.

By the phrase "antigen binding fragment" is meant at least a part of an antibody that specifically binds antigen. An example of such a fragment includes an

15   antibody V domain. Examples of a suitable V domain binding partner include a C domain and acceptable fragments thereof. Further suitable fragments include parts of the V domain having a combined molecular mass for the V domain of between from about 15 kilodaltons to about 40 kilodaltons, preferably between from about 20 kilodaltons to about 30 kilodaltons, more preferably about 25 kilodaltons as

20   determined by a variety of standard methods including SDS polyacrylamide gel electrophoresis or size exclusion chromatography using appropriately sized marker fragments, mass spectroscopy or amino acid sequence analysis. Further specific antigen binding fragments include Fab, F(v), Fab', $F(ab')_2$ and certain single-chain constructs that include the antibody V domain.

25

Additionally suitable antigen binding fragments include at least part of an antigen binding V domains alone or in combination with a cognate constant (C) domain or fragment thereof ("cognate" is used to denote relationship between two components of the same immunoglobulin heavy (H) or light (L) chain). Typical C

30   domain fragments have a molecular mass of between from about 5 kilodaltons to about 50 kilodaltons, more preferably between from about 10 kilodaltons to about 40

kilodaltons, as determined by a variety of standard methods including SDS polyacrylamide gel electrophoresis or size exclusion chromatography using appropriately sized marker fragments, mass spectroscopy or amino acid sequence analysis. Additionally suitable antigen binding fragments are disclosed below as well

5   as in U.S. Pat. Nos. 5,986,065 and 6,555,319 to Wong, H. *et al.* and PCT/US98/04644 (WO 98/40408). See also U.S. Patent Application Publication No. 20030082636 and the following International Applications: WO 03/037911 and WO 98/40408.

10

As also mentioned, one approach to minimize any potential immunorejection by primate hosts such as human patients is to make a chimeric antibody. By the phrase "chimeric antibody" or related phrase including plural forms is meant antibodies as disclosed herein whose light and heavy chain genes have been

15   constructed, typically by genetic engineering, from immunoglobulin gene segments belonging to different species, usually a primate and preferably a human. For example, the variable (V) domains of the genes from a mouse antibody such as H36 may be joined to human constant (C) domains, such as γ_1, γ_2, γ_3, or γ_4. A typical therapeutic chimeric antibody is thus a hybrid protein consisting of the V or antigen-

20   binding domain from a mouse antibody and the C or effector domain from a human antibody, although other mammalian species may be used. A specifically preferred chimeric antibody for use with the invention is the anti-tissue factor antibody cH36 disclosed below in the Examples.

25   Suitable chimeric antibodies for use with the invention can be made by one or a combination of known strategies. As disclosed in the U.S. Pat. Nos. 5,986,065, 6,555,319 and PCT/US98/04644 (WO 98/40408), a highly useful murine anti-TF antibody can be readily obtained from a variety of sources including the American Type Culture Collection (ATCC, 10801 University Boulevard, Manassas, VA

30   20110). The antibody has been deposited as ATCC Accession No. HB-12255. Alternatively, suitable antibodies can be made *de novo* (as polyclonal or monoclonal

as needed) in accord with procedures disclosed in the U.S. Pat. Nos. 5,986,065 and 6,555,319 for instance.

See also U.S. Patent Application Publication No. 20030082636 and the
5   following International Applications: WO 03/037911 and WO 98/40408.

The antibody deposited with the ATCC H36 is referred to herein as H36. It is also referenced as H36.D2 and as H36.D2.B7. The antibody designated as H36 is the antibody produced by the mother clone, and H36.D2 is obtained from the primary
10   clone, whereas H36.D2.B7 is obtained from the secondary clone. No differences were observed between the antibody produced by those three clones with respect to the antibody's ability to inhibit TF or other physical properties. In general usage, H36 is often used to indicate anti-TF antibody produced by any of these clones or related cell lines producing the antibody. The mouse-human chimeric version of H36
15   is referred to cH36 (and also as Sunol-cH36). See also the U.S. Pat. No. 5,986,065 and PCT/US98/04644 (WO 98/40408) for more specific information about the H36 antibody.

A preferred chimeric antibody combines the murine variable domain from a
20   suitable antibody such as H36 and a human constant domain. The manipulation is usually achieved by using standard nucleic acid recombination techniques. A variety of types of such chimeric antibodies can be prepared, including e.g. by producing human variable domain chimeras, in which parts of the variable domains, especially conserved regions of the antigen-binding domain, are of human origin and only the
25   hypervariable regions are of non-human origin. See S.L. Morrison, *Science*, **229**:1202-1207 (1985); Oi *et al.*, *BioTechniques* **4**:214 (1986); Teng *et al.*, *Proc. Natl. Acad. Sci. U.S.A.*, **80**:7308-7312 (1983); Kozobor *et al.*, *Immunology Today* **4**:72-79 (1983); Olsson *et al.*, *Meth. Enzymol.* **92**:3-16 (1983); U.S. Pat. No. 5,986,065; and PCT/US98/04644 (WO 98/40408).
30

Nucleic acids encoding the H36 variable and constant regions have been disclosed in the U.S. Pat. No. 5,986,065; and PCT/US98/04644 (WO 98/40408), for example. See also U.S. Patent Application Publication No. 20030082636; WO 03/037911 and WO 98/40408.

5

In one embodiment, the anti-TF chimeric antibody will include a human light chain constant (C) domain i.e., Cκ, Cλ or a fragment thereof. Often, the humanized light chain fragment will have an amino acid length of between from about 80 to about 250 amino acids, preferably between from about 95 to about 235 amino acids, more preferably between from about 104 to about 225 amino acids. The size of the humanized light chain fragment can be determined by a variety of standard methods including SDS polyacrylamide gel electrophoresis or size exclusion chromatography using appropriately sized marker fragments, mass spectroscopy or amino acid sequence analysis.

15

Typically, the chimeric antibody for use in the present methods further includes a human heavy chain variable (V) domain having an amino acid length of between about 80 to about 650 amino acids, preferably between from about 95 to about 540 amino acids, more preferably about 102 to about 527 amino acids as determined e.g., by standard SDS polyacrylamide gel electrophoresis or size exclusion chromatography using appropriately sized marker fragments, mass spectroscopy or amino acid sequence analysis.

Nucleic acid sequence encoding suitable human light chain C and V domains have been reported. See e.g., Kabat et al. in Sequences of Proteins of Immunological Interest Fifth Edition, U.S. Dept. of Health and Human Services, U.S. Government Printing Office (1991) NIH Publication No. 91-3242; and GenBank. See the National Center for Biotechnology Information (NCBI)- Genetic Sequence Data Bank (Genbank) at the National Library of Medicine, 38A, 8N05, Rockville Pike, Bethesda, MD 20894. See Benson, D.A. et al., Nucl. Acids. Res. 25:1 (1997) for a more specific description of Genbank.

Suitable recombinant techniques for use in making the chimeric antibodies and other antibodies and fragments as reported herein have been disclosed. See generally Sambrook *et al.* in *Molecular Cloning: A Laboratory Manual* (2d ed. 5   1989); and Ausubel *et al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, (1989).

For some invention applications in which a minimal immunoresponse against an anti-TF antibody is needed, it will be useful to prepare humanized antibodies. By 10   the phrase "humanized" is meant an immunoglobulin that includes at least one human FR subset, preferably at least two or three of same, more preferably four human FR subsets, and one or more CDRs from a non-human source, usually rodent such as a rat or mouse immunoglobulin. Typically preferred humanized immunoglobulins of the invention will include two or more preferably three CDRs. Constant domains 15   need not be present but are often useful in assisting function of humanized antibodies intended for *in vivo* use. Preferred constant domains, if present, are substantially identical to human immunoglobulin constant domains *i.e.*, at least about 90% identical with regard to the amino acid sequence, preferably at least about 95% identical or greater. Accordingly, nearly all parts of the humanized immunoglobulin, 20   with the possible exception of the CDRs, are preferably substantially identical to corresponding parts of naturally occurring human immunoglobulin sequences.

Methods for determining amino acid sequence identity are standard in the field and include visual inspection as well as computer-assisted approaches using 25   BLAST and FASTA (available from the National Library of Medicine (USA) website). Preferred matching programs for most embodiments are available from website for the international ImMunoGeneTics (IMGT) database and a more preferred matching program for this embodiment is the program called Match which is available in the Kabat database. See Johnson G, Wu T. "Kabat database and its 30   application: Future directions." *Nucleic Acids Res.* **29**:205-206 (2001).

By the phrase "humanized antibody" is meant an antibody that includes a humanized light chain and a humanized heavy chain immunoglobulin. See S.L. Morrison, *supra*; Oi *et al.*, *supra*; Teng *et al.*, *supra*; Kozbor *et al.*, *supra*; Olsson *et al.*, *supra*; and other references cited previously. Accordingly, a "humanized

5   antibody fragment" means a part of that antibody, preferably a part that binds antigen specifically.

The H36 or cH36 antibody can be humanized by one or a combination of approaches as described, for example, in U.S Pat. Nos. 5,766,886; 5,693,762;

10   5,985,279; 5,225,539; EP-A-0239400; 5,985,279 and 5,639,641, or as disclosed in the published U.S. application number 20030190705. See also E. Padlan *Mol. Immunol.* **28**:489 (1991); Jones *et al.*, *Nature* **321**:522-525 (1986); Junghans *et al.*, *supra*; and Roguska, *et al. PNAS (USA)* **91**:969 (1994) for additional information on humanizing antibodies.

15

Particular humanized antibodies and fragments thereof for use with the present invention are disclosed below in the Examples section.

Preferred chimeric antibodies, humanized antibodies, as well as fragments

20   thereof that specifically bind human TF. By the term, "specific binding" or a similar term is meant a molecule disclosed herein which binds another molecule, thereby forming a specific binding pair. However, the molecule does not recognize or bind to other molecules as determined by, *e.g.*, Western blotting ELISA, RIA, mobility shift assay, enzyme-immunoassay, competitive assays, saturation assays or other protein

25   binding assays know in the art. See generally, Sambrook *et al.* in *Molecular Cloning: A Laboratory Manual* (2nd ed. 1989); and Ausubel *et al.*, supra; and Harlow and Lane in *Antibodies: A Laboratory Manual* (1988) Cold Spring Harbor, New York for examples of methods for detecting specific binding between molecules.

30   Especially suitable chimeric antibodies, humanized antibodies and fragments for use with the invention will feature at least one of: 1) a dissociation constant (K_d)

for the TF of less than about 0.5 nM; and 2) an affinity constant (K_a) for the TF of less than about 10×10^{10} M^{-1}. Methods of preforming such assays are known in the field and include Enzyme-Linked Immuno-Sorbent Assay (ELISA), Enzyme ImmunoAssay (EIA) radioimmunoassay (RIA) and BIAcore analysis.

5

Additionally suitable antibodies will increase survival time in what is sometimes referred to herein as a "standard *in vivo* septic shock assay". Generally, such an assay involves administering gram-negative bacteria to monkeys to induce sepsis. See Taylor *et al. J. Clin. Invest.* **79**:918 (1987). More specifically, a dose of

10   *E. coli* (about 10^{10} CFU/kg) is freshly prepared and administered intravenously to a primate, *e.g.* baboon or rhesus monkey, in a 1-2 hour interval. A control group can receive a saline or PBS injection. The treatment group receives a bolus injection of at least 1 mg/kg antibody, preferably about 10 mg/kg prior to infusion of bacteria *e.g.*, less than about 1 hour before. Control and treatment group monkeys are then

15   monitored for about a week and checked for survival. See the Examples below for more specific information about the standard *in vivo* septic shock assay.

A preferred method of the invention employs a humanized antibody, chimeric antibody or fragment that increases monkey survival time (hours or days) by at least

20   about 2-fold, preferably at least about 3 fold, more preferably at least about 5 fold to 10 fold or more as determined by the standard *in vivo* septic shock assay.

Additionally suitable antibodies for use with the invention can attenuate (reduce presence of at least one of interleukin-6 (IL-6) and interleukin-8 (IL-8) in the

25   plasma of subject mammals after at least about 5 hours following administration of the antibody. Methods for detecting IL-6 and IL-8 and quantifying same from plasma are known and include immunological approaches such as RIA, EIA, ELISA and the like.

30   In one approach, sepsis is induced in a suitable primate such as a monkey and preferably a baboon along lines previously mentioned. Prior to inoculation of control

baboon (with about 10^{10} CFU/kg *E. coli* or saline), the treatment baboons receive a
bolus injection of at least 1 mg/kg antibody, preferably about 10 mg/kg prior to
infusion of bacteria *e.g.*, less than about 1 hour before injection of the inoculum.
Baboon survival and IL-6 and IL-8 levels in plasma are monitored by standard
5   procedures.

In another approach, a sepsis-like condition is induced in a suitable primate,
such as baboon, using a model described as a "primed sepsis model" (see Welty-
Wolf, K. *et al. Am. J. Respir. Crit. Care Med.* **164**:1988 (2001) and described in
10 further detail in Example 4).

Additionally preferred humanized antibodies, chimeric antibodies and
fragments thereof exhibit a blood clotting time of between from about 50 to about
350 seconds as determined by a standard prothrombin (PT) time assay, particularly
15 after about 5 minutes administration of the antibody or fragment to the mammal. An
especially useful PT assay has been disclosed in the U.S. Pat. Nos. 5,986,065,
6,555,319 and PCT/US98/04644 (WO 98/40408), for example.

Further preferred antibodies for use in accord with the present invention
20 inhibit platelet deposition by at least about 50% as determined by a standard platelet
deposition assay. Methods for performing the assay have been disclosed, *e.g.*, in the
pending U.S. Pat. application 10/310,113.

Still further preferred antibodies inhibit collagen-induced arthritis in an
25 experimental mouse model. See Example 5.

"Antibody", "antibody for use with the invention" and like phrases refer to
whole immunoglobulin as well as immunologically active fragments which bind a
desired antigen. The immunoglobulins and immunologically active (antigen-binding)
30 fragments thereof include an epitope-binding site (*i.e.*, a site or epitope capable of
being specifically bound by an antibody recognizing antigen). Exemplary antibody

fragments include, for example, Fab, F(v), Fab', F(ab')$_2$ fragments, "half molecules" derived by reducing the disulfide bonds of immunoglobulins, single chain immunoglobulins, or other suitable antigen binding fragments (see e.g., Bird et al., Science, 242:423-426 (1988); Huston et al., PNAS, (USA), 85:5879 (1988); Webber
5   et al., Mol. Immunol., 32:249 (1995)).

       Particular chimeric or humanized antibodies of the present invention can be polyclonal or monoclonal, as needed, and may have, without limitation, an IgG1, IgG2, IgG3 or IgG4 isotype or IgA, IgD, IgE, IgM. An especially preferred antibody
10   for use with the invention has or can be manipulated to have an IgG1 (called "hOAT") or IgG4 (called "hFAT") isotype. Such antibodies can be polyclonal or monoclonal as needed to achieve the objectives of a particular invention embodiment. In some instances, single-chain antibodies such as a humanized single-chain will be preferred.
15

       Practice of the invention is applicable to a wide spectrum of mammals. Preferably, the mammal is a primate such as a monkey, chimpanzee, or a baboon. More preferably, the primate is a human patient in need of methods disclosed herein i.e., one that has or is suspected of having sepsis or a sepsis-related condition or an
20   inflammatory disorder or disease.

       As discussed above, antibodies of the invention and suitable fragments thereof can be administered to a mammal, preferably a primate such as a human, to prevent or reduce sepsis and related complications. According to one embodiment, such
25   antibodies are used with one or more pharmaceutically acceptable non-toxic carriers such as sterile water or saline, glycols such as polyethylene glycol, oils of vegetable origin, and the like. In particular, biocompatible, biodegradable lactide polymer, lactide glycolide copolymer or polyoxyethylene, polyoxypropylene copolymers may be useful excipients. Other potentially useful administration systems include
30   ethylene vinyl acetate copolymer particles, osmotic pumps, and implantable infusion systems and liposomes. If needed, one or more suitable antibodies or fragments will

be in the form of a solution or suspension (or a lyophilized form that can be reconstituted to a solution or suspension), and will preferably include approximately 0.01% to 10% (w/w) of the antibody of the present invention, preferably approximately 0.01% to 5% (w/w) of the antibody.

5

As discussed, the antibody or fragment can be administered according to the invention as the sole active agent or in combination with other known anti-sepsis therapies. For instance, such antibodies or fragments can be administered to a human patient before, during, or after intervention with one or more appropriate antibotics,

10 typically a broad spectrum intravenous antibiotic therapy. Preferred antibiotics include those known to have broad spectrum anti-microbial activity, covering gram-positive, gram-negative, and anaerobic bacteria. Thus in one embodiment, such antibiotics are given during or after administration of the antibodies and fragments disclosed herein, preferably parenterally in doses adequate to achieve bactericidal

15 serum levels. After stabilizing the patient, various recognized supportive therapies can be used to assist recovery such as administration of oxygen, intravenous fluids, and medications that increase blood pressure. Dialysis may be necessary in the event of kidney failure, and mechanical ventilation is often required if respiratory failure occurs.

20

Persons "at risk" for developing sepsis and related conditions include, but are not limited to, the very old and very young individuals. Also at risk are those with challenged immune systems such as patients infected with a DNA or RNA virus such as HIV or herpes. Nearly any bacterial organism can cause sepsis. Certain fungi and

25 (rarely) viruses may faciliate sepsis and related conditions. Generally, toxins released by the bacteria or fungus may cause direct organ (e.g., lung, kidney) or tissue damage, and may lead to low blood pressure and/or poor organ function. These toxins also produce a vigorous inflammatory response from the body which contributes to septic shock.

30

Additional risk factors include underlying illnesses, such as diabetes; hematologic cancers (lymphoma or leukemia); and other malignancies and diseases of the genitourinary system, liver or biliary system, and intestinal system. Other risk factors are recent infection, prolonged antibiotic therapy, and having been exposed to

5   a recent invasive surgical or medical procedure. Symptoms of sepsis and related conditions are known in the field and include, but are not limited to, fever, chills, lightheadedness, shortness of breath, palpitations, cool and/or pale extremities, fever, agitation, lethargy, and confusion.

10   Success of the invention in the prevention or treatment of sepsis and related conditions can be evaluated by the caregiver using one or a combination of approaches. Typically, a reduction or elimination of one or more of the foregoing symptoms can be taken as indicative that the sepsis or related condition has been addressed. Preferably, patients receiving such treatment will survive at least about 2

15   fold longer than patients who do not receive such intervention.

As discussed, the invention provides a method for reducing cytokine production in a mammal e.g., by administering to the mammal a therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment

20   thereof that binds specifically to tissue factor (TF) to form a complex. Preferably, Factor X or Factor IX binding to the complex is inhibited and the administration is sufficient to reduce the cytokine production in the mammal. Suitable humanized antibodies, chimeric antibodies and fragments thereof are disclosed herein. Acceptable methods for monitoring cytokine production in a mammal are known and

25   include specific methods outlined in the Examples section.

Therapeutic antibodies and fragments in accord with the invention can be used in parenteral or intravenous administration, particularly in the form of liquid

30   solutions. Such compositions may be conveniently administered in unit dose and may be prepared in accordance with methods known in the pharmaceutical art. See

Remington's Pharmaceutical Sciences, (Mack Publishing Co., Easton PA, (1980)). By the term "unit dose" is meant a therapeutic composition of the present invention employed in a physically discrete unit suitable as unitary dosages for a primate such as a human, each unit containing a pre-determined quantity of active material

5 calculated to produce the desired therapeutic effect in association with the required diluent or carrier. The unit dose will depend on a variety of factors including the type and severity of sepsis to be treated, general health of the individual, medical history, and the like. Precise amounts of the antibody to be administered typically will be guided by judgment of the practitioner, however, the unit dose will generally depend

10 on the route of administration and be in the range of 10 ng/kg body weight to 50 mg/kg body weight per day, more typically in the range of 100 ng/kg body weight to about 10 mg/kg body weight per day. Suitable regimens for initial administration in booster shots are also variable but are typified by an initial administration followed by repeated doses at one or more hour intervals by a subsequent injection or other

15 administration. Alternatively, continuous or intermittent intravenous infusions may be made sufficient to maintain concentrations of at least from about 10 nanomolar to 10 micromolar of the antibody (or suitable fragment) in the blood.

Antibodies and fragments for use with the invention are preferably

20 substantially pure when used in the disclosed methods and assays. References to an antibody being "substantially pure" mean an antibody or protein that has been separated from components which naturally accompany it. For example, by using standard immunoaffinity or protein A affinity purification techniques, an antibody of the invention can be purified from hybridoma or cell culture medium by using native

25 TF as an antigen or protein A resin. Similarly, native TF can be obtained in substantially pure form by using an antibody of the invention with standard immunoaffinity purification techniques. Particularly, an antibody or protein is substantially pure when at least 50% of the total protein (weight % of total protein in a given sample) is an antibody or protein of the invention. Preferably the antibody or

30 protein is at least 60 weight % of the total protein, more preferably at least 75 weight %, even more preferably at least 90 weight %, and most preferably at least 98 weight

% of the total material. Purity can be readily assayed by known methods such as SDS polyacrylamide gel electrophoresis (PAGE), column chromatography (*e.g.*, affinity chromatography, size exclusion chromatography), mass spectroscopy or HPLC analysis. Preferably, the antibodies and fragments will be used in a sterile

5   format.

The molecular weight of the antibodies of the invention will vary depending on several factors such as the intended use and whether the antibody includes a conjugated or recombinantly fused toxin, pharmaceutical, radioisotope or detectable

10   label or the like. Also the molecular weight will vary depending on nature and extent of post-translational modifications if any (such as glycosylation) to the antibody. The modifications are a function of the host used for expression with *E. coli* producing non-glycosylated antibodies and eucaryotic hosts, such as mammalian cells or plants, producing glycosylated antibodies. In general, an antibody of the invention will have

15   a molecular weight of between approximately 20 to 150kDa. Such molecular weights can be readily determined by molecular sizing methods such as SDS-PAGE followed by protein staining or Western blot analysis.

It will be apparent that the foregoing method for making the humanized cH36

20   antibody can be readily adapted to make other humanized antibodies and antigen binding fragments according to the invention.

A. Preparation Of Humanized Anti-Tissue Factor Binding Antibody

25   Preparation and use of a humanized anti-tissue factor binding antibody is described. See also Examples 1-3 below.

Briefly, preferred antibodies bind human tissue factor to form a binding complex. The tissue factor may be naturally occurring or recombinant human (rhTF).

30   Preferably, factor X or factor IX binding to the complex is inhibited. In a preferred invention embodiment, the humanized antibody has an apparent affinity constant (K_A,

M^{-1}) for the hTF of less than about 1 nM, preferably less than about 0.5 nM, more preferably between from about 0.01 nM to about 0.4 nM. See Examples 1-3, below for more information about determining affinity constants for the humanized antibodies. By "specific binding" is meant that the humanized antibodies form a

5   detectable binding complex with the TF (or rhTF) and no other antigen as determined by standard immunological techniques such as RIA, Western blot or ELISA.

More preferred humanized anti-TF binding antibodies made in accord with this invention exhibit an apparent affinity constant (K_A, M^{-1}) for native human TF of

10   at least about 1×10^8 M^{-1} as determined by surface plasmon analysis (particularly, BIACore analysis in accordance with the procedures of Example 3 which follows), more preferably at least about 5×10^8 M^{-1} as determined by surface plasmon analysis, still more preferably an apparent affinity constant (K_A, M^{-1}) for native human TF of at least about 3×10^9 M^{-1} as determined by surface plasmon resonance analysis. Such

15   substantial binding affinity of antibodies of the invention contrast sharply from much lower binding affinities of previously reported antibodies.

The nucleic acid (SEQ ID NOS. 1 and 3) and amino acid (SEQ ID NOS. 2 and 4) sequences of a particular tissue factor binding antibody that has been

20   humanized by the present methods *i.e.* H36.D2.B7. See Figures 1A and 1B of the drawings and the PCT application WO 98/40408, for instance. SEQ ID NOS. 1 and 2 are the nucleic acid and amino acid respectively of the light chain variable domain, and SEQ ID NOS. 3 and 4 are the nucleic acid and amino acid respectively of the heavy chain variable domain, with hypervariable regions (CDRs or Complementarity

25   Determining Regions) underlined in all of those sequences.

Additional tissue factor binding humanized antibodies of the invention will have substantial amino acid sequence identity to either one or both of the light chain or heavy sequences shown in Figures 1A and 1B. More particularly, such antibodies

30   include those that have at least about 70 percent homology (amino acid sequence identity) to SEQ ID NOS. 2 and/or 4, more preferably about 80 percent or more

homology to SEQ ID NOS. 2 and/or 4, still more preferably about 85, 90 or 95 percent or more homology to SEQ ID NOS. 2 and/or 4.

5   More particular tissue factor binding humanized antibodies of the invention will have high amino acid sequence identity to hypervariable regions (shown with double underlining in Figures 1A and 1B) of SEQ ID NOS. 2 and 4). Specific antibodies will have one, two or three hypervariable regions of a light chain variable domain that has high sequence identity (at least 90% or 95% amino acid sequence identity) to or be the same as one, two or three of the corresponding hypervariable

10   regions of the light chain variable domain of H36.D2.B7 (those hypervariable regions shown with underlining in Figure 1A and are the following:

1) LASQTID (SEQ ID NO. 5);

2) AATNLAD (SEQ ID NO. 6); and

3) QQVYSSPFT (SEQ ID NO. 7).

15

Additionally specific antibodies that have been humanized by the methods described herein and bind tissue factor will have one, two or three hypervariable regions of a heavy chain variable domain that have high sequence identity (at least 90% or 95% amino acid sequence identity) to or be the same as one, two or three of

20   the corresponding hypervariable regions of the heavy chain variable domain of H36.D2.B7 (those hypervariable regions shown with underlining in Figure 1B and are the following:

1) TDYNVY (SEQ ID NO. 8);

2) YIDPYNGITIYDQNFKG (SEQ ID NO. 9); and

25   3) DVTTALDF (SEQ ID NO. 10).

Certain nucleic acids encoding some or all of the antibodies or fragments disclosed herein will preferably have a length sufficient (preferably at least about 100, 200 or 250 base pairs) to bind to the sequence of SEQ ID NO. 1 and/or SEQ ID

30   NO. 3 under the following moderately stringent conditions (referred to herein as "normal stringency" conditions): use of a hybridization buffer comprising 20%

formamide in 0.9M saline/0.12M sodium citrate (6xSSC) buffer at a temperature of 37°C and remaining bound when subject to washing once with that 2xSSC buffer at 37°C.

5   More specifically, certain of the nucleic acids (preferably at least about 100, 200 or 250 base pairs) will bind to the sequence of SEQ ID NO. 1 and/or SEQ ID NO. 3 under the following highly stringent conditions (referred to herein as "high stringency" conditions): use of a hybridization buffer comprising 20% formamide in 0.9M saline/0.12M sodium citrate (6xSSC) buffer at a temperature of 42°C and

10   remaining bound when subject to washing twice with that 1xSSC buffer at 42°C.

       Suitable nucleic acids preferably comprise at least 20 base pairs, more preferably at least about 50 base pairs, and still more preferably a nucleic acid of the invention comprises at least about 100, 200, 250 or 300 base pairs.

15

       Generally preferred nucleic acids of the invention will express an antibody of the invention that exhibits the preferred binding affinities and other properties as disclosed herein. See also the U.S. Pat. No. 5,986,065 and PCT/US98/04644 (WO 98/40408) for more information.

20

       Other appropriate nucleic acids will have substantial sequence identity to either one or both of the light chain or heavy sequences shown in Figures 1A and 1B. More particularly, preferred nucleic acids will comprise a sequence that has at least about 70 percent homology (nucleotide sequence identity) to SEQ ID NOS. 1 and/or

25   3, more preferably about 80 percent or more homology to SEQ ID NOS. 1 and/or 3, still more preferably about 85, 90 or 95 percent or more homology to SEQ ID NOS. 1 and/or 3.

       Additionally specific nucleic acid sequences will have high sequence identity

30   to hypervariable regions (shown with underlining in Figures 1A and 1B) of SEQ ID NOS. 1 and 3). Such nucleic acids include those that code for an antibody light chain

variable domain and have one, two or three sequences that code for hypervariable

regions and have high sequence identity (at least 90% or 95% nucleotide sequence

identity) to or be the same as one, two or three of the sequences coding for

corresponding hypervariable regions of H36.D2.B7 (those hypervariable regions

5   shown with underlining in Figure 1A and are the following:

      1) CTGGCAAGTCAGACCATTGAT (SEQ ID NO: 11);

      2) GCTGCCACCAACTTGGCAGAT (SEQ ID NO: 12); and

      3) CAACAAGTTTACAGTTCTCCATTCACGT (SEQ ID NO: 13).

10   More specific nucleic acids also code for an antibody heavy chain variable

domain and have one, two or three sequences that code for hypervariable regions and

have high sequence identity (at least 90% or 95% sequence identity) to or be the same

as one, two or three of the sequences coding for corresponding hypervariable regions

of H36.D2.B7 (those hypervariable regions shown with underlining in Figure 1B and

15   are the following:

      1) ACTGACTACAACGTGTAC (SEQ ID NO. 14);

      2)

          TATATTGATCCTTACAATGGTATTACTATCTACGACCAGAACTTCA

          AGGGC (SEQ ID NO. 15); and

20   3) GATGTGACTACGGCCCTTGACTTC (SEQ ID NO. 16).

      More specific humanized antibodies for use with the methods of this

invention that bind TF are those in which each of framework regions (FRs) 1, 2, 3

and 4 has at least about 90% amino acid sequence identity, preferably at least about

25   95% or greater identity to the light chain FR sequences shown in Figure 3A (SEQ ID

NO.   ), preferably, the sequence shown as "LC-09" in Figure 3A. Additionally

specific humanized antibodies include a light chain constant domain having at least

about 90% amino acid sequence identity, preferably at least about 95% sequence

identity or greater to the sequence shown in Figure 5A (SEQ ID NO.   ) or Figure

30   6A (SEQ ID NO.   ).

Further specific humanized antibodies are those in which each of framework regions (FRs) 1, 2, 3 and 4 has at least about 90% amino acid sequence identity, preferably about 95% identity or greater to the heavy chain sequences shown in Figure 4A (SEQ ID NO. ▓), preferably, the sequence shown as "HC-08" in Figure

5   4A. Additional humanized antibodies have a heavy chain constant domain with at least about 90% amino acid sequence identity, preferably at least about 95% identity or greater, to sequence shown in Figure 5B (SEQ ID NO. ▓) or Figure 6B (SEQ ID NO. ▓).

10   In certain embodiments, the humanized antibody will have an IgG1 (hOAT) or IgG4 (hFAT) isotype as disclosed in the published U.S. application number 20030190705.

      Also provided by the present invention are functional fragments of the

15   humanized antibodies disclosed herein. Examples of such fragments include, but are not limited to, those that bind TF with an affinity constant (Kd) of less than about 1 nM, preferably less than about 0.5 nM, more preferably between from about 0.01 nM to about 0.4 nM. Specifically preferred are antigen binding Fab, Fab', and F(ab)$_2$ fragments.

20

      As discussed, the invention features humanized antibodies that include at least one murine complementarity determining region (CDR), *e.g.*, CDR1, CDR2, CDR3. In one invention embodiment, the antibodies bind specifically to human tissue factor (TF) to form a complex. Typically, the factor X or factor IX binding to TF or TF-

25   FVIIa and activation by TF-FVIIa thereto is inhibited. As mentioned above, preferred CDRs (light and heavy chain) are from a rodent source, typically the mouse.

      In one embodiment of the humanized antibodies of the invention, the

30   antibodies further include at least one human framework region (FR) subset. Preferably, all the FRs (light and heavy chains) are human.

In a more particular embodiment, the first CDR (CDR1) of the heavy chain hypervariable region that binds human TF is at least 90% identical to the CDR1 amino acid sequence shown in Figure 4B (SEQ ID NO.   ), preferably at least about

5   95% identical or greater to that sequence. Typically, the second CDR (CDR2) of the heavy chain hypervariable region is at least 90% identical to the CDR2 amino acid sequence shown in Figure 4C (SEQ ID NO.   ), preferably at least about 95% identical or greater. Preferably also, the third CDR (CDR3) of the heavy chain hypervariable region is at least 90% identical to the CDR3 sequence shown in Figure

10   4D (SEQ ID NO.   ), more preferably about 95% identical or greater to that sequence.

In another invention embodiment, the first CDR (CDR1) of the light chain hypervariable region that binds human TF is at least 90% identical to the CDR1

15   amino acid sequence shown in Figure 3B (SEQ ID NO.   ), preferably at least about 95% identical or greater. Typically, the second CDR (CDR2) of the light chain hypervariable region is at least 90% identical to the CDR2 amino acid sequence shown in Figure 3C (SEQ ID NO.   ), preferably about 95% identical or greater. Preferably, the third CDR (CDR3) of the light chain hypervariable region is at least

20   90% identical to the CDR3 amino acid sequence shown in Figure 3D (SEQ ID NO.   ), more preferably about 95% identical or greater to that sequence. ·

Additional humanized antibodies suitable for use with the present methods include a first framework region (FR1) of the heavy chain hypervariable region that

25   binds human TF which FR1 is at least 90% identical to the amino acid sequence shown in Figure 4A (SEQ ID NO.   ) as "FR1 HC-08", preferably about 95% identical or greater to that sequence. In one embodiment, the FR1 comprises at least one of the following amino acid changes: E1 to Q; Q5 to V; P9 to G; L11 to V; V12 to K; Q19 to R; and T24 to A. Preferably, the FR1 includes two, three, four, five, or

30   six of those changes with all of those amino acid changes being preferred for many applications.

34

Further humanized antibodies suitably bind human TF and include a second framework region (FR2) of the heavy chain hypervariable region which FR2 is at least 90% identical to the sequence shown in Figure 4A (SEQ ID NO. [ ]) as "FR2

5   HC-08", preferably about 95% identical or greater to that sequence. In one embodiment, the FR2 at least one of the following amino acid changes: H41 to P and S44 to G. A preferred FR2 includes both of those amino acid changes.

The invention also features use of humanized antibodies that bind human TF

10   in which a third framework region (FR3) of the heavy chain hypervariable region is at least 90% identical to the sequence shown in Figure 4A (SEQ ID NO. [ ]) as "FR3 HC-08", preferably about 95% identical or greater to that sequence. In one embodiment, the FR3 includes at least one of the following amino acid changes: S76 to T; T77 to S; F80 to Y; H82 to E; N84 to S; T87 to R; D89 to E and S91 to T. A

15   preferred FR3 includes two, three, four, five or six of those amino acid changes with all seven of those amino acid changes being generally preferred.

Also featured is use of humanized antibodies that suitably bind human TF and in which the fourth framework region (FR4) of the heavy chain hypervariable region

20   is at least 90% identical to the amino acid sequence shown in Figure 4A (SEQ ID No. [ ]) as "FR4 HC-08", preferably at least about 95% identical or greater to that sequence. Preferably, the FR4 includes the following amino acid change: L113 to V.

Additional humanized antibodies bind human TF and also feature a first

25   framework region (FR1) of the light chain hypervariable region which is at least about 90% identical to the amino acid sequence shown in Figure 3A (SEQ ID NO. [ ]) as "FR1 LC-09", preferably at least about 95% identical or greater to that sequence. In one embodiment, the FR1 comprises at least one of the following amino acid changes: Q11 to L; L15 to V; E17 to D; and S18 to R. A preferred FR1

30   includes two or three of such amino acid changes with all four amino acid changes being generally preferred.

The present invention also features use of humanized antibodies that bind human TF and in which a second framework region (FR2) of the light chain hypervariable region is at least about 90% identical to the amino acid sequence

5   shown in Figure 3A (SEQ ID NO. 🔲) as "FR2 LC-09", preferably at least about 95% identical or greater to that sequence. A preferred FR2 has the following amino acid change: Q37 to L.

Also encompassed by the invention is use of particular humanized antibodies

10   that bind human TF in which a third framework region (FR3) of the light chain hypervariable region is at least about 90% identical to the amino acid sequence shown in Figure 3A (SEQ ID NO. 🔲) as "FR3 LC-09", preferably at least about 95% identical or greater to that sequence. In one embodiment, the FR3 has at least one of the following amino acid changes: K70 to D, K74 to T, A80 to P, V84 to A,

15   and N85 to T. Preferably, the FR3 has two, three, or four of such amino acid changes with all five of the changes being generally preferred.

Additional humanized antibodies appropriate for use with the methods disclosed herein bind TF and include a fourth framework region (FR4) of the light

20   chain hypervariable region which FR4 is at least about 90% identical to the sequence shown in Figure 3A (SEQ ID NO. 🔲) as "FR4 LC-09", preferably at least about 95% identical or greater to that sequence. In one embodiment, the FR4 includes at least one and preferably all of the following amino acid changes: A100 to Q and L106 to I.

25

The invention also features a human TF binding fragment of the foregoing humanized antibodies. Examples of such fragments include Fab, Fab', and F(ab)₂. See the published U.S. application number 20030190705 and references cited therein for additionally preferred humanized anti-TF antibodies made in accord with this

30   invention.

The following three nucleic acid vectors pSUN36 (humanized anti-TF antibody Ig G1-HC expression vector), pSUN37 (humanized anti-TF antibody Ig G4-HC expression vector), and pSUN38 (humanized anti-TF antibody LC expression vector) have been deposited pursuant to the Budapest Treaty with the American Type

5   Culture Collection (ATCC) at 10801 University Boulevard, Manassas VA 20110-2209. The vectors were assigned the following Accession Numbers: PTA-3727 (pSUN36); PTA-3728 (pSUN37); and PTA-3729 (pSUN38).

Suitable expression and purification strategies for making and using the

10   humanized anti-TF antibodies of this invention have been disclosed in the published U.S. application number 20030190705, for instance.

As discussed, the invention also provides useful kits for performing one or more of the methods provided herein. In one embodiment, the kit includes at least

15   one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to human tissue factor (TF) to form a complex, wherein factor X or factor IX binding to the complex is inhibited. Typically also, the humanized antibody, chimeric antibody, or fragment thereof is provided in a pharmaceutically acceptable vehicle such as saline, water or buffer. The kit may include a pharmaceutically

20   acceptable vehicle for dissolving the humanized antibody, chimeric antibody or fragment prior to use.

The following non-limiting examples are illustrative of the invention. In the following examples and elsewhere the method of the invention is applied to the

25   humanization of the murine anti-tissue factor antibody H36. See the U.S Patent Nos. 5,986,065 and 6,555,319; U.S. Patent Application Publication No. 20030082636; WO 03/037911 and WO 98/40408, and the published U.S. patent application number 20030190705 and references cited therein as well as the discussion above. Sometimes, the Fab fragment of H36 or cH36 will be referred to as "H36-Fab" and

30   "cH36-Fab", respectively, for the sake of convenience.

All documents mentioned herein are fully incorporated by reference in their entirety.

EXAMPLE 1 – Humanization of Anti-Tissue Factor Antibody

5   The description of how to make and use a particular murine antibody called H36.D2 (sometimes also called H36 as discussed above) is described in U.S. Pat. Nos. 5,986,065 and 6,555,319. The present example shows how to make and use a humanized version of that antibody. A humanized H36 antibody has a variety of uses including helping to minimize potential for human anti-mouse antibody (HAMA)

10   immunological responses. These and other undesired responses pose problems for use of the H36 antibody in human therapeutic applications.

         A.   Preparation of chimeric anti-tissue factor antibody (cH36)

15   The H36 antibody described previously is an IgG2a murine antibody. H36 was first converted to a mouse-human chimeric antibody for clinical development. To do this, the heavy and light chain genes for H36 were cloned (see U.S. Patent No. 5,986,065). The heavy chain variable domain was fused to a human IgG4 constant (Fc) domain and the light chain variable domain was fused to a human kappa light

20   chain constant domain. The resulting IgG4κ chimeric antibody was designated cH36 (and is also referred to as Sunol-cH36). For multiple uses of H36 or cH36 in patients with chronic diseases, a fully humanized cH36 is preferred so that it will decease or eliminate any human anti-chimeric antibody (HACA) immunological response. The humanization of cH36 is described below.

25

         B.   Humanization Strategy for cH36 Antibody

         Humanization of the chimeric anti-tissue factor antibody cH36 was achieved by using a "FR best-fit" method of the invention. This method takes full advantage

30   of the fact that a great number of human IgGs with known amino acid sequences or sequences of human IgG fragments are available in the public database. The

sequences of the individual framework regions of the mouse heavy and light variable domains in cH36 are compared with the sequences respective heavy or light chain variable domains or human frameworks (or fragments thereof) in the Kabat database (see e.g., Kabat et al. in Sequences of Proteins of Immunological Interest Fifth

5   Edition, U.S. Dept. of Health and Human Services, U.S. Government Printing Office (1991) NIH Publication No. 91-3242 or http://immuno.bme.nwu.edu). The following criteria were used to select the desired human IgG framework region subsets for humanization: (1) The number of mismatched amino acids was kept as low as possible. (2) Amino acids inside the "vernier" zone (amino acids in this zone may

10   adjust CDR structure and fine-tune the fit to antigen, see Foote, J. and Winter, G., J. of Mol. Bio. 224(2):487-499 [1992]) were left unchanged. (3) Conservative amino acid substitutions were favored when evaluating similar candidates. The matching program used for this comparison can be found in Kabat database. See Johnson G, Wu T. "Kabat database and its application: Future directions." Nucleic Acids Res.

15   29:205-206 (2001). The program finds and aligns regions of homologies between the mouse sequences and human sequences in the Kabat's database. By using this unique FR best-fit method, it is anticipated that the humanized LC or HC variable domains of the target IgG may have all the four FRs derived from as few as one human IgG molecule or to as many as four different human IgG molecules.

20

B(i). Selection of Human IgG Kappa Light Chain Variable Domain Framework Regions

The amino acid sequence in each of the framework regions of cH36 LC was

25   compared with the amino acid sequence in the FRs in human IgG kappa light chain variable domain in Kabat Database. The best-fit FR was selected based on the three criteria described above.

The amino acid sequence of human IgG kappa light chain variable domain

30   with a Kabat Database ID No. 005191 was selected for humanization of cH36 LC

FR1. The amino acid sequence of human IgG kappa light chain variable domain with a Kabat Database ID No. 019308 was selected for humanization of cH36 LC FR2. The following mutations were made in cH36 LC FR1 to match the amino acid sequence of a human IgG kappa light chain variable domain with a Kabat Database

5   ID No. 005191: Q11 → L, L15 → V, E17 → D, S18 → R. One mutation Q37 → L was made cH36 LC FR2 to match the amino acid sequence of a human IgG kappa light chain variable domain with a Kabat Database ID No. 019308 (see Table 1A for sequence information).

10   The amino acid sequence of a human IgG kappa light chain variable domain with a Kabat Database ID No. 038233 was selected for humanization of cH36 LC FR3. The amino acid sequence of a human IgG kappa light chain variable domain with a Kabat Database ID No. 004733 was selected for humanization of cH36 LC FR4. The following mutations were made in cH36 LC FR3 to match the amino acid

15   sequence of a human IgG kappa light chain variable region with a Kabat Database ID No. 038233: K70 → D, K74 → T, A80 → P, V84 → A, N85 → T. Two mutations A100 → Q and L106 → I were made cH36 LC FR4 to match the amino acid sequence of a human IgG kappa light chain variable domain with a Kabat Database ID No. 004733 (see Table 1B for sequence information).

20

        B(ii). Selection of Human IgG Heavy Chain Variable Domain Framework Regions

        The amino acid sequence in each of the framework regions of cH36 HC was

25   compared with the amino acid sequence in the FRs in human IgG heavy chain variable domain in Kabat Database. The best-fit FR was selected based on the three criteria described above.

        The amino acid sequence of a human IgG heavy chain variable domain with a

30   Kabat Database ID No. 000042 was selected for humanization of cH36 HC FR1. The amino acid sequence of a human IgG heavy chain variable domain with a Kabat

Database ID No. 023960 was selected for humanization of cH36 HC FR2. The
following mutations were made in cH36 HC FR1 to match the amino acid sequence
of a human IgG heavy chain variable domain with a Kabat Database ID No. 000042:
E1 → Q, Q5 → V, P9 → G, L11 → V, V12 → K, Q19 → R, T24 → A. Two
5   mutations H41 → P and S44 → G were made cH36 HC FR2 to match the amino acid
sequence of a human IgG heavy chain variable domain with a Kabat Database ID No.
023960 (see Table 2A for sequence information).

The amino acid sequence of a human IgG heavy chain variable domain with a
10   Kabat Database ID No. 037010 was selected for humanization of cH36 HC FR3. The
amino acid sequence of a human IgG heavy chain variable domain with a Kabat
Database ID No. 000049 was selected for humanization of cH36 HC FR4. The
following mutations were made in cH36 HC FR3 to match the amino acid sequence
of a human IgG heavy chain variable domain with a Kabat Database ID No. 037010:
15   S76 → T, T77 → S, F80 → Y, H82 → E, N84 → S, T87 → R, D89 → E, S91 → T.
One mutations L113 → V was made cH36 HC FR2 to match the amino acid
sequence of a human IgG heavy chain variable domain with a Kabat Database ID No.
000049 (see Table 2B for sequence information).

Table 1. Comparison of cH36 and Human Light Chain (LC) FR Sequences

Table 1A

Names	LC-FR1 (23 aa)	LC-FR2 (15 aa)
	1 10 20	35 49
cH36-LC	DIQMTQSPASQSASLGESVTITC	WYQQKPGKSPQLLIY
Human-LC	L V DR	L
	005191	019308

Table 1B

Names	LC-FR3 (32 aa)	LC-FR4 (10 aa)
	57 60 70 80 88	98
cH36-LC (107)	GVPSRFSGSGSGTKFSFKISSLQAEDFVNYYC	FGAGTKLELK
Human-LC	D T P AT	Q I
	038233	004733

Table 2. Comparison of cH36 and Human Heavy Chain (HC) FR Sequences

Table 2A

Names	HC-FR1 (30 aa)	HC-FR2 (14 aa)
	1 10 20 30	36 49
cH36-HC	EIQLQQSGPELVKPGASVQVSCKTSGYSFT WVRQSHGKSLEWIG	
Human-HC	Q V G VK R A	P G
	000042	023960

Table 2B

Names	HC-FR3 (32 aa)	HC-FR4 (11 aa)
	67 75 85 95	107 117
cH36-HC	KATLTVDKSSTTAFMHLNSLTSDDSAVYFCAR	WGQGTTLTVSS
Human-HC	TS Y E S R E T	V
	037010	000049

Once the decisions on the desired human framework regions were made, the following three techniques were used to achieve the desired amino acid substitutions in both the light and heavy chains: (1) Regular PCR was used for cloning, to introduce cloning or diagnostic restriction endonuclease sites, and to change amino acid residues located at the ends of the variable domains. (2) PCR-based mutagenesis

42

was used to change multiple amino acid residues at a time, especially when these residues were in the middle of the variable domains. (3) Site-directed mutagenesis was used to introduce one or two amino acid substitutions at a time. Site-directed mutagenesis was done following the protocol described in Stratagene's

5   "QuickChange Site-Directed Mutagenesis Kit" (Catalog #200518).

After each step, the partially humanized clones were sequenced and some of these variable domains were later cloned into expression vectors. The plasmid tKMC180 was used to express LC mutants, and the pJRS 355 or pLAM 356 vector

10   was used to express HC mutants as IgG1 or IgG4, respectively. Some of these clones were then combined and expressed transiently in COS cells to determine the expression levels by ELISA.

The final fully humanized forms of the anti-TF heavy and light variable

15   domains were cloned into what is sometimes referred to herein as a "mega vector" and transfected into CHO and NSO cells for IgG expression. Stable cell lines were then used to produce amounts of humanized anti-TF sufficient for analysis. The resulting humanized versions are 100% human in origin (when the CDR sequences are not considered). The humanized IgG4 kappa version is designated hFAT

20   (humanized IgG Four Anti-Tissue Factor antibody) and the IgG1 kappa version is designated hOAT (humanized IgG One Anti-Tissue Factor antibody). These fully humanized versions of cH36 are intended for treating chronic indications, such as thrombosis, cancer and inflammatory diseases.

25   C. Generation of Humanized Anti-TF Antibody Heavy Chain

       1. PCR amplification and cloning into pGem T-easy of anti-TF mAb cH36
          heavy chain (HC) variable domain were performed using plasmid
          pJAIgG4TF.A8 (an expression vector for chimeric H36) as template and

30   primers TFHC1s2 and TFHC1as2. Primer TFHC1s2 introduced a *BsiW*1 site
          upstream of the initiation codon and also an amino acid change E1 to Q in

framework (FR) 1. Primer TFHC1as introduced an amino acid change **L113** to V in FR4. This step resulted in the construct **HC01**.

2. PCR-based mutagenesis using the previous construct (HC01) and the following four primers generated construct **HC02**. Upstream PCR used primers TFHC1s2 and TFHC7as. Downstream PCR used primers TFHC7s and TFHC1as2. PCR using upstream and downstream PCR products as templates and with primers TFHC1s2 and TFHC1as2 yielded **HC02**. The use of primers TFHC7s and TFHC7as introduced two amino acid changes in FR2: **H41** to P and **S44** to G.

3. PCR-based mutagenesis using HC02 as template and the following four primers generated construct **HC03**. Upstream PCR used primers TFHC1s2 and TFHC5as2. Downstream PCR used primers TFHC5s and TFHC1as2. PCR using upstream and downstream PCR products as templates and with primers TFHC1s2 and TFHC1as2 yielded **HC03**. The use of primers TFHC5s and TFHC5as2 introduced three amino acid changes in FR3: **T87** to R, **D89** to E, and **S91** to T. A *Bgl* II site was also introduced at position. 87.

4. PCR amplification was performed using primers TFHC2s and TFHC3as and HC03 in pGem as template. TFHC2s sits upstream of the cloning site in pGem. TFHC3as sits in framework 3 and introduces two amino acid changes in FR3: **H82** to E and **N84** to S. The resulting PCR band was cloned into pGem and then the proper size insert was digested with *BsiW*1 and *Bgl* II. Cloning of this fragment into **HC03** yields **HC04**.

5. PCR-based mutagenesis using **HC04** as template and the following primers resulted in **HC05**. Upstream PCR used primers TFHC1s2 and TFHC6as. Downstream PCR used primers TFHC6s and TFHC1as2. Mutagenic PCR using upstream and downstream PCR products as templates and with primers

TFHC1s2 and TFHC1as2 yielded **HC05**. This step introduced the following amino acid changes in FR3: **S76** to T, **T77** to S, and **F80** toY.

6. PCR-based mutagenesis using **HC05** as template and the following four primers generated **HC06**. Upstream PCR used primers TFHC2s and TFHC2as2. Downstream PCR used primers TFHC3s2 and TFHC1as2. Amplification using TFHC2as2 introduced an amino acid change in FR1: **P9** to G. Primer TFHC3s2 changes **Q19** to R and **T24** to A. PCR using upstream and downstream PCR products as template and with primers TFHC1s2 and TFHC1as2 yielded **HC06.**

7. A point mutation from I to M in position 2 of FR1 was spontaneously introduced during construction of **HC06**. PCR amplification using **HC06** as template and TFHC1s3 and TFHC1as2 as primers, corrected this erroneous substitution and also introduced an amino acid. change in FR1: **Q5** to V. The resulting construct was **HC07**.

8. Construct **HC08** was made by PCR-based mutagenesis using **HC07** as template and the following primers. TFHC2s and TFHC2as3 were used for the upstream product. The downstream product was previously amplified using TFHC1s3 and TFHC1as2 (see step 7). The use of primer TFHC2as3 introduced two amino acid changes in FR1: **L11** to V and **V12** to K. A spontaneous point mutation resulted in a phenylalanine to leucine (F → L) change at position 64 in CDR2. Further screening and sequencing yielded construct **HC08R1**, which has the correct sequence of F at position 64 in CDR2.

9. Two constructs, **HC11** and **HC12**, were generated by site-directed mutagenesis from **HC07**. Two complementary primers TFHC8sP and TFHC8asP were used along with **HC07** as template to produce **HC11** which contains three amino acid changes in FR1: **G9** to P, **L11** to V, and **V12** to K.

45

Then, **HC11** was methylated and column purified for the next round of site directed mutagenesis. PCR using **HC11** as a template and the complementary primers TFHC9sL and TFHC0asL generated **HC12** which has a mutation from **V11** to L in FR1.

5

10. Construct **HC09** was derived from **HC12** by performing PCR using **HC12** as a template and the complementary primers TFHC10sK and TFHC10asK. **HC09** contains an amino acid change: **K12** to V in FR1.

10   11. Construct **HC10** was made from **HC09**. PCR using **HC09** as a template and the complementary primers LV-1 and LV-2 resulted in the generation of **HC10**, which contains a mutation from **L11** to V in FR1.

After each mutation step, the partially humanized or fully humanized clones were

15   sequenced and some of these variable domains were later cloned into expression vectors. pJRS 355 or pLAM 356 vector was used to express HC mutants fused to Fc of human IgG1 or IgG4.

Figures 3A-D summarize steps 1-11 and shows incremental amino acid changes

20   introduced into FR1-4. Except HC08, all other heavy chain mutants and cH36 contain F at position 64 in CDR2. HC08 has a mutation from F to L at·position 64. Figures 4B-D show the heavy chain CDR sequences.

Primers Used for Heavy Chain Humanization

25

TFHC1s2
5' TTTCGTACGTCTTGTCCCAGATCCAGCTGCAGCAGTC 3'

TFHC1as2
30   5' AGCGAATTCTGAGGAGACTGTGACAGTGGTGCCTTGGCCCCAG 3'

TFHC7s
5' GTGAGGCAGAGCCCTGGAAAGGGCCTTGAGTGGATTGG 3'

35   TFHC7as

5' CCAATCCACTCAAGGCCCTTTCCAGGGCTCTGCCTCAC 3'

TFHC5s
5'GCATCTCAACAGCCTGAGATCTGAAGACACTGCAGTTTATTTCTGTG 3'

5

TFHC5as2
5' CTGCAGTGTCTTCAGATCTCAGGCTGTTGAGATGCATGAAGGC 3'

TFHC3as
10   5' GTCTTCAGATCTCAGGCTGCTGAGCTCCATGAAGGCTGTGGTG 3'

TFHC2s
5' TACGACTCACTATAGGGCGAATTGG 3'

15   TFHC6s
5' CTGTTGACAAGTCTACCAGCACAGCCTACATGGAGCTCAGCAG 3'

TFHC6as
5' CTGCTGAGCTCCATGTAGGCTGTGCTGGTAGACTTGTCAACAG 3'

20

TFHC2as2
5' GCACTGAAGCCCCAGGCTTCACCAGCTCACCTCCAGACTGCTGCAGC 3'

TFHC3s2
25   5'CTGGGGCTTCAGTGCGGGTATCCTGCAAGGCTTCTGGTTACTCATTCAC
3'

TFHC1s3
5' TCGTACGTCTTGTCCCAGATCCAGCTGGTGCAGTCTGGAGGTGAGC 3'

30

TFHC2as3
5' GCACTGAAGCCCCAGGCTTCTTCACCTCACCTCCAGACTGCACC 3'

TFHC9sL
35   5' GCAGTCTGGACCTGAGCTGAAGAAGCCTGGGG 3'

TFHC9asL
5' CCCCAGGCTTCTTCAGCTCAGGTCCAGACTGC 3'

40   TFHC8sP
5' GCTGGTGCAGTCTGGACCTGAGGTGAAGAAGCC 3'

TFHC8asP
5' GGCTTCTTCACCTCAGGTCCAGACTGCACCAGC3'

45

TFHC10sK

5' GCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTC 3'

TFHC10asK
5' GAAGCCCCAGGCTTCACCAGCTCAGGTCCAGACTGC 3'

5

LV-1
5' CAGTCTGGACCTGAGGTGGTGAAGCCTGGG 3'

LV-2
10   5' CCCAGGCTTCACCACCTCAGGTCCAGACTG 3'

D. Generation of Humanized Anti-TF Antibody Light Chain

15   1. PCR amplification was performed using plasmid pJAIgG4TF.A8 (an expression
          vector for chimeric H36) as template and primers TFLC1s2.1 and TFLC1as2.
          This step introduced a cloning site, *Age*I, upstream of the coding region. It also
          introduced the **L106I** mutation in FR4. This step yielded the construct **LC03**.

20   2. Site-directed mutagenesis was performed using complementary primers TFLC5s
          and TFLC5as and LC03 as template. This step introduced the mutation **Q37L** in
          FR2 and added a *Pst*I site for diagnostic purposes. This new construct is named
          LC04.

25   3. PCR amplification was performed using **LC04** as template and primers TFHC2s
          and TFLC2as1. This step generated **Fragment A** that will be used in step 6. This
          step introduced **Q11L** and **L15V** mutations in FR1.

      4. PCR amplification was performed using **LC04** as template and primers
30   TFLC1s2.1 and TFLC1asR. This introduced the *Kpn*I site at the end of LC
          variable domain. Cloning of this PCR fragment into pGEM yields **pGEM04K**
          that will be used in step 6.

      5. PCR amplification was performed using **LC04** as template and primers TFLC2s
35   and TFLC4as. This step generated **Fragment C** that will be used in step 6.

Three mutations **E17D, S18R** in FR1 and **A100Q** in FR4 were introduced in this step.

6. PCR-based mutagenesis using **Fragment A** and **Fragment C** as templates and primers TFHC2s and TFLC4as yielded **Fragment D**. Cloning of **Fragment D** into pGEM04K yielded the construct **LC05**.

7. PCR amplification was performed using pGEM04K as template and primers TFLC1s2.1 and TFLC4as. This step generated **Fragment H**, which is then cloned into pGEM04K. This introduced the **A100Q** mutation in FR4 and the construct is named **LC06**.

8. PCR amplification was performed using **LC06** as template and primers TFLC1s2.1 and TFLC3as. This step generated **Fragment I** that will be used in step 10. This introduced the **K70D** and the **K74T** mutations in FR3.

9. PCR amplification was performed using **LC06** as template and primers TFLC3s2 and TFLC4as. This step generated **Fragment F** that will be used in step 10. This introduced the **A80P** mutation in FR3.

10. PCR using **Fragment I** and **Fragment F** as templates and primers TFLC1s2.1 and TFLC4as yielded **Fragment J**. Cloning of **Fragment J** into pGEM yielded the construct **LC07**.

11. Site-directed mutagenesis was conduced using complementary primers TFLC08sds and TFLC08sdsa and **LC07** as template. This step introduced the mutations **V84A** and **N85T** in FR3. This construct is named **LC08**.

12. The *Age*I to *Eco*O109I fragment from **LC05** containing the mutations **Q11L, L15V, E17D, S18R** and **Q37L** is cloned into **LC08**. This yielded the construct **LC09**.

13. Site-directed mutagenesis was conduced using **LC09** as template and the complementary primers LC105 and LC103. This step introduced the **T85N** mutation in FR3 and yielded the construct **LC10**.

5

14. Site-directed mutagenesis was conducted using **LC10** as template and the complementary primers LC115 and LC113. This step introduced the **D70K** mutation in FR3. This yielded the construct **LC11**.

10

15. Site-directed mutagenesis was conducted using **LC11** as template and the complementary primers LC125a and LC123a. This step introduced the **K42Q** mutation in FR2. This yielded the construct **LC12**.

After each mutation step, the partially humanized or fully humanized LC clones were sequenced and some of these variable domains were later cloned into expression vector tKMC180.

Oligonucleotide Primers Used for Light Chain Humanization

20   TFLC1as2:
5' TTCGAAAAGTGTACTTACGTTTGATCTCCAGCTTGGTCCCAG 3'

TFLC1s2.1:
5' ACCGGTGATATCCAGATGACCCAGTCTCC 3'

25

TFLC5s:
5' GGTTAGCATGGTATCTGCAGAAACCAGGG 3'

TFLC5as:
30   5' CCCTGGTTTCTGCAGATACCATGCTAACC 3'

TFHC2s:
5' TACGACTCACTATAGGGCGAATTGG 3'

35   TFLC2as1:
5' CCACAGATGCAGACAGGGAGGCAGGAGACTG 3'

TFLC1asR:
5'
TTCGAAAAGTGTACTTACGTTTGATCTCCAGCTTGGTACCAGCACCGAAC
G 3'

5

TFLC2s:
5' CCTGTCTGCATCTGTGGGAGATAGGGTCACCATCACATGC 3'

TFLC4as:
10   5' GATCTCCAGCTTGGTACCCTGACCGAACGTGAATGG 3'

TFLC3as:
5' GTAGGCTGCTGATCGTGAAAGAAAGTCTGTGCCAGATCC 3'

15   TFLC3s2:
5' CACGATCAGCAGCCTACAGCCTGAAGATTTTGTAAATTATTACTGTC 3'

TFLC08sds:
5' GCAGCCTACAGCCTGAAGATTTTGCAACTTATTACTGTCAACAAG 3'

20

TFLC08sdsa:
5' CTTGTTGACAGTAATAAGTTGCAAAATCTTCAGGCTGTAGGCTGC 3'

LC105:
25   5' CAGCAGCCTACAGCCTGAAGATTTTGCAAATTATTACTGTCAAC 3'

LC103:
5' GTTGACAGTAATAATTTGCAAAATCTTCAGGCTGTAGGCTGCTG 3'

30   LC115:
5' CAGTGGATCTGGCACAAAGTTTTCTTTCACGATCAGCAGC 3'

LC113:
5' GCTGCTGATCGTGAAAGAAAACTTTGTGCCAGATCCACTG 3'

35

LC125a:
5' CTGCAGAACCAGGGCAATCTCCTCAGCTCCTG 3'

LC123a:
40   5' CAGGAGCTGAGGAGATTGCCCTGGTTCTGCAG 3'

Figure 5A shows the sequence of the human kappa light chain constant
domain (SEQ ID NO. _____) . Figure 5B shows the human IgG1 heavy chain

51

constant domain (SEQ ID NO. ___). Figure 6A shows the hFAT (IgG4) constant
domain sequence (SEQ ID NO. ___). Figure 6B provides the human IgG4 heavy
chain constant domain (SEQ ID NO. ___). See also the published U.S. patent
application number 20030190705 and references cited therein for additional
5   disclosure relating to the foregoing immunoglobulin constant domain sequences.

EXAMPLE 2 – Expression and Purification of Humanized anti-TF Antibodies

10   The partially humanized or fully humanized LC and HC clones were cloned
into expression vectors. The plasmid tKMC18 was used to express LC mutants fused
to human kappa chain, and pJRS 355 or pLAM 356 vector was used to express HC
mutants fused to Fc of human IgG1 or IgG4. Some combinations of the HC and LC
clones were then co-transfected into COS cells. The transiently expressed IgGs in
15   COS cells were assayed for the whole IgG production and binding to TF by ELISA.
For disclosure relating to these particular vectors see the published U.S. patent
application number 20030190705 and references cited therein.

           The final fully humanized forms of the anti-TF heavy and light variable
20   domains (combination of HC08 and LC09) were cloned into what is referred to as a
Mega expression vector (pSUN34, see Figure 2) and transfected into CHO and NSO
cells for IgG expression. Stably transfected cell lines producing the IgG4κ or IgG1κ
humanized anti-TF antibody were cloned. The selected stable cell lines were then
used to produce amounts of humanized anti-TF sufficient for analysis. The resulting
25   humanized versions are approximately 100% human in origin (when the CDR
sequences are not considered). The humanized IgG4 kappa version (produced by
pSUN35) is designated hFAT (humanized IgG Four Anti-Tissue Factor antibody) and
the IgG1 kappa version (produced by pSUN34) is designated hOAT (humanized IgG
One Anti-Tissue Factor antibody). These fully humanized versions of cH36 are
30   intended for treating chronic indications, such as cancer and inflammatory diseases.

One of the NSO cell lines (OAT-NSO-P10A7) that expresses (combination of HC08 and LC09) was thawed and extended in 10 mL of IMDM medium supplemented with 10% FBS in a 15 mL tube and centrifuged. The cell pellet was resuspended in 10 mL of fresh media and passed to a T25 flask and incubated at 37°C

5   in 5% CO_2. In order to prepare a sufficient number of cells to inoculate a hollow fiber bioreactor, the cells were expanded to obtain a total of $6x10^8$ cells. A bioreactor was set up as per manufacturer's instruction manual. The harvested cells were pelleted and resuspended in 60 mL of IMDM containing 35% FBS and injected into the extracapillary space of the bioreactor. Concentrations of glucose and lactate were

10 monitored daily and the harvest material was centrifuged and pooled. The harvested material was tested for anti-TF antibody concentrations by ELISA assay. The pooled sample containing anti-TF antibody (hFAT) were then purified and analyzed as described below.

15   A. rProtein A Sepharose Fast Flow Chromatography

Recombinant humanized anti-TF monoclonal antibody consists of two light and two heavy chains. Heavy chain is a fusion of mouse variable domain (unaltered or humanized as described above) and human IgG1 or IgG4 Fc domain, while light

20 chain contains mouse variable domain (unaltered or humanized as described above) and human κ domain. It is well established that human IgG Fc region has high affinity for Protein A or recombinant Protein A (rProtein A).

Harvest pools containing humanized anti-TF antibody (hFAT) were adjusted

25 to pH 8.0 ± 0.1 by adding 0.08 ml of 1 M Tris-HCl, pH 8.0 per ml of sample. Then the sample is filtered through low protein-binding 0.22 micron filters (e.g., Nalgene sterile disposable tissue culture filter units with polyethersulfone membrane from Nalge Nunc International, Cat. No. 167-0020). Following sample application, rProtein A column (from Pharmacia) is washed with 5 bed volumes of 20 mM Tris-

30 HCl, pH 8.0 to remove unbound materials such as media proteins. Since the harvest medium contains high content of bovine serum, a stepwise pH gradient wash was

used to remove bovine IgG from the column. The stepwise pH gradient was achieved by increasing the relative percentage of Buffer B (100 mM acetic acid) in Buffer A (100 mM sodium acetate). A typical pH stepwise wash employed 20%, 40%, and 60% Buffer B. Elute the column with 100% Buffer B and collect fractions based on

5   A_{280}. The pooled fractions were adjusted to pH 8.5 with addition of 1 M Tris base.

B. Q Sepharose Fast Flow Chromatography

Anion ion exchange chromatography is very effective in separating proteins

10   according to their charges. The eluted and pH-adjusted sample from rProtein A column was diluted with two volumes of water, and the pH is checked and adjusted to 8.5. The sample was then loaded to a 5 ml (1.6 x 2.5 cm) Q Sepharose Fast Flow equilibrated with 20 mM Tris-HCl, pH 8.5 and the column washed with (1) 5 bed volumes of 20 mM Tris-HCl, pH 8.5; and (2) 4 bed volumes of 20 mM Tris-HCl, pH

15   8.5 containing 100 mM NaCl. The IgG protein was then eluted with bed volumes of 20 mM Tris-HCl, pH 8.5 containing 500 mM NaCl. The protein peaks were pooled and buffer-exchanged into PBS using ultrafiltration device.

20   **EXAMPLE 3**: Septic Shock Model in Rhesus Monkeys

In this model, septic shock was induced by infusion of live *E. coli*, a gram-negative bacterium (see Taylor *et al.*, J. Clin. Invest. **79**:918-825 (1987)) in rhesus monkeys. The shock induced by *E. coli* causes activation both coagulation and

25   inflammation, ultimately leading to death. The ability of an anti-TF antibody of the present invention to prolong the survival times of rhesus monkeys treated with live *E. coli* was examined using the rhesus model of septic shock described by Taylor *et al.*, *supra*. Rhesus monkeys weighing 3-5 kilograms were fasted overnight before study and immobilized the morning of the experiment with ketamine hydrochloride (14

30   mg/kg, intramuscularly). Sodium pentobarbital was then administered in the cephalic vein through a percutaneous catheter to maintain a light level of surgical anesthesia (2 mg/kg initially and with additional amounts approximately every 20 to 45 minutes for

54

6 hours). A femoral vein was exposed aseptically and cannulated in one hind limb for sampling blood and administering gentamicin. Gentamicin was administrated by means of 30-minute intravenous infusions. An infusion of 9 mg/kg was administrated at the end of *E. coli* infusion (t = 2 hours). An infusion of 4.5 mg/kg was administrated 6 hours after *E. coli* infusion. Additional gentamicin (4.5 mg/kg, i.m.) was administrated once daily after day 1 for 3 more days. Each monkey was placed on its side in contact with controlled-temperature heating pads and rectal temperature was monitored. Animals were intubated orally and allowed to breathe spontaneously.

The *E. coli* strain O86:K61H (ATCC 33985) was freshly prepared in less than 12 hours prior to injection. Each monkey received a 2-hour intravenous infusion of *E. coli* at a dose of 4×10^{10} CFU/kg. Control group monkeys received PBS 30 minutes before infusion of *E. coli*. Treatment group monkeys received a bolus (2-3 minutes) dose of anti-tissue factor antibody (cH36, diluted in PBS if necessary) 30 minutes before infusion of *E. coli* (see Timeline for injection schedule). The percutaneous catheter was used to infuse *E. coli*, PBS and anti-TF antibody.

Timeline for anti-TF antibody and *E. coli* administration.

All monkeys were monitored continuously for 8 hours and observed daily for a maximum of 7 days, for the following: survival time: monitored and recorded hourly; temperature was measured and recorded hourly for the first 8 hours and then once a day for up to 7 days.

Blood samples were collected at the following time points: T = -0.5*, 0**, 1, 2, 4, 6, 24 hours as shown in Table 3 for the analysis of hematological references and inflammatory cytokines. (*T = -0.5, right before injection of cH36 or saline control; **T = 0, right before infusion of *E coli* but 30 min after injection of cH36 or saline control).

Table 3. The schedule for collecting blood samples.

Time Point	Hematology	Plasma for Analysis
Day 1; t = -0.5 hr (just prior to test article or vehicle infusion)	X	X
Day 1; t = 0 hour (30 minutes after treatment, just prior to E. coli infusion)	X	X
Day 1; 1 hour (following E. coli infusion	X	X
Day 1; 2 hour (following E. coli infusion)	X	X
Day 1; 4 hour (following E. coli infusion)	X	X
Day 1; 6 hour (following E. coli infusion)	X	X
Day 1; 24 hour (following E. coli infusion)	X	X
Volume of whole blood / time point	1.0 mL	1.8 mL
Anticoagulant	EDTA	Sodium Citrate

The results of this study are shown in Table 4 and Fig.7A-D. Anti-TF antibody cH36 protected rhesus monkeys very well from E. coli-induced septic shock when administered as a10 mg/kg bolus injected intravenously (Table 4), while

5   attenuating inflammatory cytokines IL-8 and IL-1β, and to a lesser extent IL-6 and TNF-α (Fig. 7A-D).

Table 4. Protective Effect of cH36 on E coli-induced Septic Shock in Rhesus Monkeys

Treatment	Weight (kg)	Sex	Survival Time (hr)	Average Survival Time (hr)
Saline	3.6 4.5	F M	8 24	16
Sunol-cH36 (10 mg/kg)	3.1 4.0	F M	>168 54	>111

10

EXAMPLE 4: Acute Lung Injury Model in Baboons

A. Acute lung injury is an important cause of morbidity and mortality in

15   sepsis. Patients infected with gram-negative sepsis have a high incidence of acute respiratory distress syndrome and multiple organ failure. It has been shown that blocking tissue factor function with active site-inactivated factor VIIa could limit

sepsis-induced acute lung injury and other organ damage in baboons (see Welty-Wolf, K. *et al.*, *Am. J. Respir. Crit. Care Med.* 164:1988 (2001)). A critical pathophysiological feature of the acute respiratory distress syndrome (ARDS) is local activation of extrinsic coagulation and inhibition of fibrinolysis. As the injury

5   evolves, these perturbations cause deposition of fibrin in the microvascular, interstitial and alveolar spaces of the lung leading to capillary obliteration and hyaline membrane formation. Components of the extrinsic coagulation pathway such as TF, thrombin and fibrin signal alterations in inflammatory cell traffic and increases in vascular permeability. Procoagulants and fibrin also promote other key events in the

10   injury including complement activation, production of proinflammatory cytokines, inhibition of fibrinolysis, and remodeling of the injured lung. It has been established that sepsis-induced TF expression activates the extrinsic coagulation cascade in the lung and leads to a procoagulant environment, which results in fibrin deposition and potentiates inflammation. By blockade of the initiating events of extrinsic

15   coagulation, their effects on proinflammatory events in the lungs and disordered fibrin turnover may be corrected and the evolution of severe structural and functional injury may be averted during experimental ARDS. Recent studies demonstrated that preventing initiation of coagulation at TF-Factor VIIa complex with active site inhibited factor VIIa (FVIIai) or TF pathway inhibitor (TFPI) attenuates fibrin

20   deposition and inflammation in sepsis, thereby limiting acute lung injury (ALI) and other organ damage in baboons.

A model for sepsis-induced ALI model has been established in baboons. See Welty-Wolf, K. *et al.*, *Am. J. Respir. Crit. Care Med.* 164:1988 (2001). In this

25   model, hyperdynamic cardiovascular and systemic inflammatory responses are pre-activated by a priming infusion of killed *E. coli*. After 12 hours, a second dose of live *E. coli* is given to the animals to induce pulmonary and renal failure similar to humans with sepsis and ARDS. Using this model, blockade of TF function by FVIIai and TFPI was shown to attenuate systemic inflammatory responses, decrease fibrin

30   deposition in tissues, and prevented lung and renal injury.

In this model, overnight fasted, adult baboons (*Papio cyanocephalus*) were
sedated with intramuscular ketamine (20-25 mg/kg) and intubated. Heavy sedation
was maintained with ketamine (3-10 mg/kg/h) and diazepam (0.4-0.8 mg/kg every 2
hours). Animals were mechanically ventilated (21% O_2) with a volume-cycled

5   ventilator and paralyzed intermittently with pancuronium (4 mg intravenously) before
respiratory measurements. An indwelling arterial line and a pulmonary artery
catheter were placed via femoral cut down for hemodynamic monitoring. All animals
received approximately 10^9 CFU/kg heat-killed *E. coli* 086:K61H (ATCC 33985) as a
60 min infusion at t = 0 h, 12 h before live *E. coli*. Sepsis was induced at t = 12 h by

10 infusing 10^{10} CFU/kg of live *E. coli* in a volume of 50 mL over 60 min. Gentamicin
(3 mg/kg i.v.) and Ceftazidime (1 gm i.v.) were administered 60 min after completion
of the live *E. coli* infusion. Fluids were given as needed to maintain pulmonary
capillary wedge pressure (PCWP) at 8-12 mmHg and to support blood pressure.
Dopamine was used for hypotension when mean arterial pressure (MAP) fell below

15 65 mmHg despite fluids. After 48 h (36 h after the live bacteria infusion) animals
were deeply anesthetized and killed by KCl injection. Physiologic parameters
including heart rate (HR), temperature, arterial blood pressure, pulmonary artery
pressure, ventilator parameters, and fluid intake were recorded every hour.
Measurements were obtained every six hours of cardiac output (CO) by

20 thermodilution, central venous pressure (CVP), PCWP, arterial and mixed venous
blood gases, oxygen saturation, oxygen content and hemoglobin (Hgb) as reported.
Urinary catheter output was measured every six hours and fluid balance calculated as
total i.v. fluid intake minus urine output.

25   Treatment efficacy for each intervention were assessed by comparing the
responses of drug-treated animals with vehicle-treated animals using the
physiological, histologic, and biochemical endpoints of lung injury listed below:

- Physiological endpoints were evaluated as the alveolar-to-arterial O_2 difference
  ($AaDo_2$), pulmonary system compliance (C_L), pulmonary artery pressures,
30   pulmonary vascular resistance (PVR) and tissue W/D ratios. Secondary

endpoints were fluid volume requirements, serum HCO_3, V_E at constant $PaCO_2$, urine output, creatinine, and systemic DO_2, VO_2 and VCO_2.

- Pathologic endpoints analyzed were gross tissue appearance and qualitative light microscopic analysis, including fibrin deposition, in lung, kidney, adrenal, and
5   other tissues.

- Biochemical endpoints were tissue myeloperoxidase (MPO) levels, total tissue and lavage protein, and lavage LDH. Lung and small bowel edema were measured by wet/dry weights.

Blood samples were drawn at 0, 12, 13, 18, 24, 36, and 48 h. Plasma (from citrated
10   blood) and serum were separated and stored at -80° C. Plasma samples were assayed for interleukin (IL) 6 and IL 8 using ELISA kits (R and D Systems, Inc., Minneapolis, MN).

The experimental protocol is summarized in Table 5.
15

Table 5. Experimental Protocol

Time (hours)	0	6	12	14	18	24	30	36	42	48		
Heat-killed *E. coli*	X											
Live *E. coli*			X									
Antibiotics				X								
Vehicle or drug				X	X	X	X	X	X	X		
Studies*	X	X	X	X	X	X	X	X	X	X		
Sacrifice										X		

*Studies include serum, plasma, urine and physiology measurements outlined in the detailed methods.

TF blockade was done using a total antibody dose of 3.5 mg/kg for the cH36 Fab and 5.25 mg/kg for cH36. The intravenous loading dose of test article (1.8 mg/kg for cH36 Fab or 2.7 mg/kg for cH36) was begun 2 hours after infusion of live microorganisms, at the time antibiotics were administered, followed by a constant 34-hour infusion of 50 mcg/kg per hour for cH36 Fab or 75 mcg/kg/hour for cH36.

Table 6. Experimental Design

Group	Treatment	# Animals
1	Sepsis + vehicle	5
2	Sepsis + cH36 Fab (3.5 mg/kg total, 1.8 mg/kg loading, 50 mcg/kg/hr infusion for 34 hr)	2
3	Sepsis + Sunol-cH36 (5.25 mg/kg total, 2.7 mg/kg loading, 75 mcg/kg/hr infusion for 34 hr)	5

TF blockade with bolus injection of cH36, followed by infusion, attenuated systemic expression of the proinflammatory cytokine IL-8 and IL-6 to a lesser extent (Figs. 11A-B), and provided partial renal and lung protection in baboons challenged with *E. coli*. Interim analysis indicates that cH36 administration attenuates increases in mean pulmonary artery pressure, lung system compliance (Figs. 8A-B) and in the alveolar-arterial oxygen gradient. The kidneys in the animals examined thus far appeared grossly normal at necropsy, the

kidney myeloperoxidase levels remained lower (Figure 9A) and urine output was maintained throughout the experiments. The small bowel wet/dry ratio in the treated animals was significantly lower that in the control animals indicative of less edema in the cH36 treated animals (Figure 9B).

These data indicate that coagulation blockade targeting TF with Sunol-cH36 prevents inflammation and the development of organ injury in gram-negative sepsis. These data also show, for the first time, a new strategy for management of ARDS in humans with anticoagulant.

B. The following data further show that cH36 and cH36-Fab are useful in preventing lung injury in septic baboons.

Briefly, the objective of this part of the example is to further confirm effects of Sunol-cH36 and cH36-Fab on procoagulant-fibrinolytic balance and inflammation in the lung and relate them to the structural and gas exchange abnormalities in ALI in an experimental sepsis model in baboons. See section A, above.

All baboons (*Papio cyanocephalus*) were mechanically ventilated (21% O_2), anesthetized, and given a dose of heat-killed *E. coli* (1×10^9 CFU/kg) intravenously 12 hours prior to the onset of live *E. coli* sepsis ($1-2 \times 10^{10}$ CFU/kg). The study design consisted of three groups of baboons as shown in Table 7, below. The baboons in the first group (n=6) were administered vehicle (PBS) and served as controls. The animals in the second group (n=3) were injected with cH36-Fab (3.5 mg/kg total, 1.8 mg/kg bolus loading dose followed by constant infusion of 50 mcg/kg/hr for 34 hours). The third group (n=6) received cH36 (5.25 mg/kg total, 2.7 mg/kg bolus loading dose followed by a constant infusion of 75 mcg/kg/hr for 34 hours). The intravenous loading dose of drug (1.8 mg/kg for cH36-Fab or 2.7 mg/kg for cH36) was started 2 hours after infusion of live microorganisms (at the 14-hour time point) followed by a constant infusion of 50 mcg/kg per hour for cH36-Fab or 75 mcg/kg/hour for cH36 until the end of the experiment at 48 hours. Antibiotics were administered at the 14-hour time point. Treatment efficacy was assessed by comparison of the responses of the treated animals with the controls using physiological, histological and biochemical parameters of lung injury.

Table 7.   Experimental Design

Group	Treatment	No. of Baboons
1	Sepsis + vehicle	6
2	Sepsis + cH36-Fab (3.5 mg/kg total, 1.8 mg/kg loading, 50 mcg/kg/hr infusion for 34 hr)	3
3	Sepsis + cH36 (5.25 mg/kg total, 2.7 mg/kg loading, 75 mcg/kg/hr infusion for 34 hr)	6

From the foregoing data, it can be concluded that animals treated with cH36 had a less hyperdynamic systemic response to sepsis.

The following Materials and Methods were used as needed to conduct the experiments in this Example. They were also used elsewhere in this disclosure as indicated .

C. Materials and Methods

Mechanically ventilated (21% O_2), anesthetized baboons (*Papio cyanocephalus*) were given a dose of heat-killed *E. coli* (1 x 10^9 CFU/kg) intravenously 12 hours prior to the onset of live *E. coli* sepsis (1-2 x 10^{10} CFU/kg). The intravenous loading dose of drug (1.8 mg/kg for cH36-Fab or 2.7 mg/kg for cH36) was started 2 hours after infusion of live microorganisms (14 hours), at the time antibiotics were administered, followed by a constant infusion of 50 mcg/kg per hour for cH36-Fab or 75 mcg/kg/hour for cH36. The total antibody dose was 3.5 mg/kg for the cH36-Fab and 5.25 mg/kg for cH36. Treatment was initiated after the onset of gram-negative sepsis because we have previously shown that TF blockade is effective as a rescue strategy. Because initial studies suggested greater efficacy and no harmful effects of whole antibody compared to Fab, comparisons were made between untreated sepsis controls and septic animals treated with cH36 whole antibody. Experimental groups are as shown in Table 7. Statistical analyses used ANOVA for physiologic data and t test or Mann Whitney U for biochemical and BAL data. Data are expressed as mean ± sem and p values are shown.

Animals were handled in accordance with appropriate guidelines. The animals
were divided randomly into treatment and sepsis control groups. After an overnight
fast, each animal was sedated with intramuscular ketamine (20-25 mg/kg) and
intubated. Heavy sedation was maintained with ketamine (3-10 mg/kg/h) and
5   diazepam (0.4-0.8 mg/kg every 2 hours). Animals were ventilated with a volume-
cycled ventilator and paralyzed intermittently with pancuronium (4 mg intravenously)
before respiratory measurements. The FiO_2 was 0.21, tidal volume 12 ml/kg, positive
end-expiratory pressure 2.5 cm H_2O, and a rate adjusted to maintain an arterial PCO_2
of 40 mmHg. An indwelling arterial line and a pulmonary artery catheter were
10   placed via femoral cut down for hemodynamic monitoring. The animals received
gentamicin sulfate (3 mg/kg iv) and ceftazidime (1 gm iv) two hours after the start of
live E. coli infusion (14 hours). The animals were supported with intravenous volume
infusion (Ringer's lactate) at a rate sufficient to maintain the pulmonary capillary
wedge pressure (PCWP) at 8 to 12 mmHg. Dopamine was used if needed to maintain
15   mean arterial pressure of 60 mmHg. After 48 h (36 h after the live bacteria infusion)
animals were deeply anesthetized and killed by KCl injection. Predefined early
termination criteria included refractory hypotension (MAP less than 60 mmHg
despite dopamine and adequate PCWP), hypoxemia (need for FIO_2 greater than
40%), or refractory metabolic acidosis (pH < 7.10 with normal $PaCO_2$). The
20   experimental protocol was the same as that shown in Table 5, above.

Physiological parameters including heart rate (HR), temperature, arterial
blood pressure, pulmonary artery pressure, ventilator parameters, and fluid intake
were recorded every hour. Measurements were obtained every six hours of cardiac
25   output (CO) by thermodilution, central venous pressure (CVP), PCWP, arterial and
mixed venous blood gases, oxygen saturation, oxygen content and hemoglobin (Hgb).
Urinary catheter output was measured every six hours and fluid balance calculated as
total iv. fluid intake minus urine output.

30   Blood samples were drawn at 0, 12, 13, 18, 24, 36, and 48 h. Complete blood

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counts were performed on whole blood (Sysmex-1000 Hemocytometer; Sysmex, Inc.,
Long Grove, IL). Plasma (from citrated blood) and serum were separated and stored
at –80°C. Fibrinogen was measured using an ST4 mechanical coagulation analyzer
(Diagnostica Stago, Parsippany, NJ). Prothrombin time (PT) and activated partial

5   thromboplastin time (aPTT) were measured in duplicate, and antithrombin III (ATIII)
activity was measured on an MDA coagulation analyzer (Organon Teknika, Durham,
NC) with a chromogenic assay and expressed as % of the kit standard. ELISA was
used to measure plasma thrombin-antithrombin (TAT) complexes (Dade Behring,
Deerfield, IL) in plasma and BAL. cH36 and cH36-Fab levels in blood and BAL

10   were measured by Sunol Molecular (Miramar, FL). Serum samples were assayed for
interleukin 1β (IL-1β), IL-6, IL-8, and TNF receptor-1 (TNFR-1) using ELISA kits
(R and D Systems, Inc., Minneapolis, MN). Blood creatinine was measured with
standard clinical techniques.

15   Tissues were collected at autopsy as follows: After the experiments the
thorax was opened, the left mainstem bronchus ligated, and the left lung removed.
BAL was performed on the left upper lobe with 240 mL 0.9% saline. Samples of
lung tissue from the left lower lobe were manually inflated and immersed in 4%
paraformaldehyde for light microscopy. Four samples were taken at random from the

20   remainder of the left lung for wet/dry weight determination taking care to avoid large
vascular and bronchial structures. Additional samples from lung, kidney, liver, small
bowel, heart, and adrenal were flash frozen in liquid nitrogen and stored at –80°C.
The entire right lung was inflation-fixed for 15 min at 30 cm fixative pressure with
2% glutaraldehyde in 0.85 M Na cacodylate buffer (pH 7.4). Additional tissue from

25   kidney, liver, small bowel, heart, and adrenal was fixed by immersion in 4%
paraformaldehye. Four samples of small bowel were selected randomly for wet/dry
weight determination.

         Myeloperoxidase (MPO) activity and protein concentration of lung

30   homogenates and protein and lactate dehydrogenase (LDH) concentrations of BAL

fluid were measured as described (*Am J Resp Crit Care Med* 1998;157:938). MPO activity was expressed as a change in absorbance/min/g wet weight tissue. LDH values were expressed in units of activity per liter (U/L).

5   An important objective of the following Examples was to determine the effects of cH36 and cH36-Fab on procoagulant-fibrinolytic balance and inflammation in the lung. It was also an objective to correlate these parameters to the structural and gas exchange abnormalities in ALI in an experimental sepsis model in baboons.

10   **D. Results:** Treatment with cH36 prevents fibrinogen depletion in baboons with *E. coli* sepsis.

15   Briefly, cH36 treatment attenuated fibrinogen depletion and TAT complex formation, consistent with inhibition of TF-dependent activation of coagulation. In sepsis controls, fibrinogen decreased to approximately 50% of initial values, but in animals treated with cH36 mean fibrinogen levels did not drop below baseline values (Figure 10A, $p < 0.01$ versus sepsis controls). PT increased in sepsis controls during

20   sepsis due to a progressive coagulopathy, and also increased in treated animals due to pharmacologic effect of the drug infusion. PT and fibrinogen values in the three cH36-Fab treated animals are also shown for comparison. The decreased values in the cH36-Fab compared to whole antibody treated animals suggest that the Fab fragment has a lower affinity for TF (Figure 10A,B). PTT increased in both groups

25   and was not significantly different. TAT complexes increased after infusion of live bacteria in both groups, peaking at 14 h and then decreasing. Peak TAT value was lower and levels decreased more rapidly in animals treated with cH36 (Figure 10D, $p < 0.01$). The difference in TAT complex formation was not due to differences in ATIII levels, as ATIII decreased similarly in the two groups, to 35-40% of initial

30   values by the end of the experiment.

E. Results: Treatment with Sunol-cH36 attenuates sepsis-induced acute lung injury

cH36 decreased ALI in baboons with established *E. coli* sepsis, attenuating sepsis-induced abnormalities in gas exchange, pulmonary hypertension, and loss of pulmonary system compliance. These physiologic data are shown in Figures 8A-C. Alveolar arterial oxygen gradient ($AaDO_2$, mmHg) increased in both groups after infusion of killed bacteria and progressively worsened in the sepsis control group after the onset of live bacterial sepsis at t = 12 h. Compared to septic control animals, treatment with cH36 prevented progressive deterioration in gas exchange during sepsis (p = 0.001, Figure 8A). One animal in the sepsis control group required supplemental oxygen after the onset of live bacterial sepsis for progressive hypoxemia. One animal in the cH36 treated group also required oxygen, but only from 18-22 hours, during which oxygenation gradually improved and supplemental O_2 was weaned back to room air. At the end of the experiment the $AaDO_2$ in that animal had recovered to initial values measured prior to infusion of heat-killed or live bacteria. Sepsis-induced increase in mean pulmonary artery pressure (PAM, mmHg) was attenuated by cH36 (p < 0.0001 vs. untreated sepsis controls, Fig 8B) but there was no difference in pulmonary vascular resistance, suggesting that this was due to effect on cardiac output in the treated animals. cH36 also prevented the decrease in pulmonary system compliance (Cst in mL/cm H_2O) seen in sepsis control animals (p < 0.01, Fig 8C). The $PaCO_2$ was controlled within the normal range, between 35-45 mmHg in both groups, but was slightly higher in sepsis controls (p=0.03) despite 20% higher minute ventilation (V_E, l/min, p=0.015), suggesting cH36 attenuated sepsis-induced increases in dead space (Table 7).

At post-mortem, the lungs from sepsis control animals were dense and hemorrhagic. The gross appearance of the lungs from animals treated with cH36 was improved and in some animals appeared the same as lungs from normal uninjured baboons. Lung wet/dry weights were not significantly different in the two groups, 6.32 ± 0.66 in septic controls compared to 5.57 ± 0.34 in cH36 treated animals (p = NS, normal reference range is 4.6-5.0). BAL protein and LDH were also not significantly different between the two groups. BAL protein was 1.0 ± 0.3 in septic

controls compared to 1.0± 0.4 in cH36 treated animals, and LDH was 23.9 ± 10.6 in septic controls compared to 10.6 ± 3 in cH36 treated animals. Neutrophil accumulation, as measured by myeloperoxidase (MPO) activity (OD/min/gm wet wt), was decreased over 40% in cH36 treated animals (p=0.07).

Lung histology showed protection in septic animals treated with cH36. The lungs of sepsis control animals had thickened alveolar septae, patchy alveolar edema and hemorrhage, and intra-alveolar inflammatory cell infiltration with macrophages and PMNs. Lungs of treated animals had improved alveolar septal architecture, decreased alveolar PMN infiltration, less alveolar edema, and no alveolar hemorrhage.

EXAMPLE 5: Treatment with cH36 improves renal function and reduces organ injury in sepsis

Materials and methods used to perform the present Example have been desribed previously. See eg., Example 4.

Treatment with cH36 improved renal function in sepsis. Urine output was significantly higher after infusion of live *E. coli* in animals treated with cH36 compared to untreated controls (p < 0.001). This was not due to differences in resuscitation because fluid balance and systemic hemodynamics were similar in the two groups. Blood pH and serum [HCO3⁻] were lower in untreated animals (both p < 0.0001), and values were consistent with mixed metabolic and respiratory acidosis in sepsis controls. Serum creatinine was not different in the two groups at the end of the experiments, and there was variability in the treated group due to one animal that was not protected.

See Figures 13A-C (showing mean urine output (13A), mean blood pH (13B), and serum bicarbonate levels (13C) with control and cH36 antibodies.

Kidneys from untreated animals were swollen and hemorrhagic at post mortem but appeared more normal in cH36 treated animals. H&E stained sections of the

kidneys of untreated animals had patchy to extensive areas of acute tubular necrosis (ATN) and glomerular damage. The kidneys of treated animals, except for a few small foci of ATN, showed normal renal architecture. MPO values were significantly decreased in kidneys from treated animals (p=0.01).

5   Other organ injury was also improved in the cH36 treated animals. Adrenals from untreated animals were swollen and hemorrhagic and small bowel was grossly edematous. In contrast, adrenals and small bowel appeared almost normal in animals treated with cH36. Small bowel wet/dry weights were decreased in septic animals treated with cH36 (6.46 ± 0.62 in Sunol-cH36 treated vs. 9.70 ± 1.05 in untreated

10   sepsis control animals, p = 0.01). Histology confirmed improvement in small bowel edema. Adrenals were also protected from sepsis, with decrease in congestion and hemorrhage, and areas of cellular damage were markedly diminished. In addition to the decreased neutrophil content in the lung and kidney, cH36 treatment significantly decreased PMN content in the liver (p=0.05,), and histology showed decreased injury

15   to hepatocytes.

        EXAMPLE 6: cH36 treatment attenuated sepsis-induced anemia

20   Materials and methods used to perform the present Example have been explained above. See eg., Example 4.

        Both groups of animals developed neutropenia, thrombocytopenia and anemia after infusion of live *E. coli* (see Table 8, below). Hemoglobin (Hgb) decreased in

25   both groups but was significantly higher in septic animals treated with cH36 (8.1 ± 0.7 versus 10.8 ± 0.8 g/dL at 48 hours, p < 0.0001). Although platelets declined more rapidly in untreated animals (p<0.0001), the clinical significance of this difference is not clear. All animals developed progressive thrombocytopenia after the infusion of live *E. coli* and mean platelet counts were approximately 30,000 or less in both

30   groups at the end of the experiment. WBC reached a nadir of approximately 1,000-1,500 (x $10^3/\mu L$) in both groups two hours after the infusion (t = 14 h) and

progressively increased to baseline levels by the end of the experiment (12,680 ± 2,012 in treated vs. 10,500 ± 1,336 in untreated animals, p = 0.07). Two sepsis control animals developed self-limited hematuria. Most animals in both groups had some blood tinged secretions associated with suctioning at some point in the study,

5   but there was no clinical evidence of significant hemorrhage (*i.e.* hematuria, hemoptysis, or bleeding from intravenous or arterial catheter sites) in the cH36 treated animals and no severe or life-threatening bleeding complications occurred in either group.

Table 8

10

Time (h)		0	12	18	24	36	48	p value
Hgb (g/dL)								
	Sepsis	11.2 ± 0.3	10.6 ± 0.3	10.4 ± 0.5	10 4 ± 0.8	8.7 ± 0.8	8.1 ± 0.7	
	cH36	12.1 ± 0.5	11.8 ± 0.4	12.2 ± 0.5	12.4 ± 0.6	10.9 ± 0.8	10.8 ± 0.8	<0.0001
	cH36 Fab	11.7 ± 0.3	11.5 ± 0.5	12.5 ± 0.8	11.4 ± 0.3	11.3 ± 0.4	9.6 ± 0.1	
Platelets								
	Sepsis	194 ± 15	126 ± 12	59 ± 7	33 ± 5	24 ± 5	26 ± 9	
	-cH36	206 ± 15	167 ± 16	110 ± 13	64 ± 12	40 ± 4	30 ± 4	<0.0001
	cH36 Fab	197 ± 8	146 ± 4	87 ± 10	31 ± 5	21 ± 4	25	
HR (beats/min)								
	Sepsis	95 ± 6	116 ± 10	125 ± 9	129 ± 9	125 ± 5	127 ± 16	
	cH36	84 ± 3	101 ± 4	135 ± 13	123 ± 11	105 ± 12	99 ± 9	<0.01
	cH36 Fab	75 ± 7	89 ± 9	107 ± 14	109 ± 9	98 ± 15	98 ± 9	
MAP (mmHg)								
	Sepsis	111 ± 2	104 ± 2	99 ± 9	102 ± 7	79 ± 10	78 ± 13	
	cH36	102 ± 3	93 ± 3	97 ± 5	92 ± 6	78 ± 9	86 ± 5	NS
	cH36 Fab	108 ± 4	85 ± 4	89 ± 9	78 ± 8	89 ± 4	63 ± 4	
CO/kg								
	Sepsis	0.16 ± 0.01	0.20 ± 0.02	0.23 ± 0.04	0.22 ± 0.03	0.22 ± 0.04	0.23 ± 0.02	
	cH36	0.15 ± 0.01	0.18 ± 0.01	0.16 ± 0.02	0.16 ± 0.02	0.15 ± 0.02	0.18 ± 0.01	<0.0001
	cH36 Fab	0.12 ± 0.01	0.14 ± 0.01	0.12 ± 0.01	0.15 ± 0.01	0.14 ± 0.01	0.14 ± 0.02	
D_{O2}/kg								
	Sepsis	23.2 ± 2.2	28.1 ± 3.1	28.6 ± 4.1	26.2 ± 2 0	22.7 ± 24.3	20.1 ± 1.2	
	cH36	23.8 ± 1.8	28.0 ± 1.0	23.8 ± 2.4	24.9 ± 3.5	23.1 ± 2.6	24.6 ± 2.1	NS
	cH36 Fab	18.1 ± 1.6	21.8 ± 2.1	19.5 ± 1.8	20.9 ± 2.7	21.1 ± 1.8	16.4 ± 1.4	
V_{O2}/kg								
	Sepsis	5 4 ± 0.8	6.3 ± 1.4	6.7 ± 0.6	6.8 ± 1.3	5.7 ± 0.6	5.6 ± 0.7	
	cH36	5.6 ± 0.4	6.6 ± 0.2	6.2 ± 0.4	5.6 ± 0.7	6.1 ± 0.6	6.2 ± 0.3	NS
	cH36 Fab	4.0 ± 0.3	4.2 ± 0.2	3.7 ± 0.4	4.6 ± 0.3	3.7 ± 0.2	4.2 ± 0.2	
SVR*kg								
	Sepsis	56602 ± 5459	41539 ± 5049	35290 ± 4941	37788 ± 5675	30713 ± 9152	26161 ± 5750	
	cH36	50833 ± 3782	37936 ± 895	49953 ± 8998	46811 ± 6290	37432 ± 3612	36058 ± 4362	***
	cH36 Fab	69095 ± 2475	43890 ± 5700	52763 ± 7023	39545 ± 7126	46570 ± 5101	32243 ± 8576	
PCWP								
	Sepsis	10 ± 1	11 ± 1	10 ± 1	11 ± 1	12 ± 1	11 ± 1	
	cH36	10 ± 0	10 ± 0	9 ± 1	9 ± 1	11 ± 2	9 ± 1	NS
	cH36 Fab	12 ± 0	14 ± 1	10 ± 1	10 ± 1	11 ± 1	12 ± 2	
V_E								
	Sepsis	3.5 ± 0.3	3.5 ± 0.2	3.8 ± 0.2	4.2 ± 0.2	5 0 ± 0.5	5.1 ± 0.4	
	cH36	3.7 ± 0.1	3.9 ± 0.2	4.0 ± 0.2	4 3 ± 0.2	4 4 ± 0.3	4.3 ± 0.2	=0.015

cH36 (ng/mL)			15 hr				
cH36 Fab	4 3 ± 0 2	4 4 ± 0.2	4.5 ± 0.1	5.0 ± 0.4	6.4 ± 0.8	6.2 ± 0.9
cH36	0	49.3 ± 5.5	51.8 ± 3.3	60.2 ± 6.0	53.0 ± 5.6	58.0 ± 8.3
cH36 Fab	0	±	±	±	±	±

Clinical and histological evaluations are performed to confirm that anti-tissue factor injections inhibited the development of rheumatoid arthritis in these mice.

Referring to the foregoing Examples and discussion, it was found that animals treated with cH36 had a less hyperdynamic systemic response to sepsis. Most systemic hemodynamic measurements, including mean arterial pressure (MAP), PCWP, systemic vascular resistance*kg (SVR*kg), VO_2, and DO_2, were not altered by treatment with cH36 (Table 8). Hypotension responded to IV fluids and dopamine infusion in both groups. Nine of the 12 animals survived until the scheduled termination point of the protocol. Overall, septic animals treated with cH36 were less hyperdynamic, without further increases in cardiac output (CO/kg) after the onset of live bacterial sepsis, and had less tachycardia and higher systemic vascular resistance*kg (SVR*kg) at the end of the experiment (Table 7, for instance). In some instances, treated animals needed dopamine and fluid support as did the untreated controls and MAP and SVR were not detectably different between the two groups. Survival is not intended for use as an endpoint as all animals were sacrificed at the 48 hour time point. Three septic animals were treated with cH36-Fab to assess for differences between whole antibody and Fab fragment. As expected, the whole antibody was often more effective then the Fab fragment.

EXAMPLE 7: Impact of cH36 on pro-inflammatory cytokine levels

Cytokine levels were measured in serum and BAL fluid along lines already described above (eg., Example 5). In the circulation, cH36 treatment attenuated IL-8 ($p<0.01$, Fig. 12) but had no detectable effect on IL-1β, or TNFR-1. In BAL fluid, cH36 attenuated elevations in IL-6, IL-8 and TNFR-1. BAL cytokine levels are shown in Table 9 below. We also measured soluble thrombomodulin (sTM) and found no differences in treated vs. untreated animals in serum or BAL. The data

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show that inhibiting coagulation using Sunol-cH36 to block the FX binding site on TF-FVIIa complex attenuates acute lung injury at least in part through effects on proinflammatory cytokine levels in the alveolar compartment. This could be an effect on local cytokine production and/or leakage of proteins from the circulation

5   across the alveolar epithelium.

Table 9. BAL cytokine levels

	Sepsis control	Sunol-cH36	p value	cH36-Fab
IL-6 (pg/mL)	600 ± 269	506 ± 522	0.05	1159 ± 435
IL-8 (pg/mL)	1081± 448	224 ±176	0.037	1478 ± 755
IL-1β (pg/mL)	6.9 ± 1.5	7.9 ± 3.1	NS	8.5 ± 1.8
TNFR1 (pg/mL)	294 ±126	107 ± 31	0.09	167 ± 93
sTM (ng/mL)	1.67 ± 0.54	0.9 ± 0.11	NS	2.17 ± 0.72

10
Certain results from Examples 4-7 can be summarized as follows:

Most systemic hemodynamic measurements, including mean arterial pressure (MAP), oxygen consumption (VO$_2$/kg), and oxygen delivery (DO$_2$/kg), were not altered by treatment with cH36 (Table 8). Mean pulmonary capillary wedge

15   pressure (PCWP) was slightly higher in sepsis control animals (p<0.01) but both groups were within the set parameters of the study. Systemic vascular resistance*kg (SVR*kg) was slightly higher in treated animals (p< 0.05, Table 3). Hypotension responded to IV fluids and dopamine infusion in both groups. Nine of the 12 animals survived until the scheduled termination point of the protocol. Two sepsis control

20   animals died prior to scheduled termination from ALI, with refractory hypoxemia and respiratory acidosis, one at 30 hours and one at 38 hours. One animal in the H36 group was not protected and died at 36 hours of refractory hypotension and metabolic acidosis. In that animal, lack of protection correlated with lower drug levels. Overall, septic animals treated with cH36 were less hyperdynamic, without further increases

25   in cardiac output (CO/kg) after the onset of live bacterial sepsis, and had less tachycardia and higher systemic vascular resistance per kg (SVR*kg) at the end of the experiment (Table 7).

EXAMPLE 8: Treatment of Baboons with cH36-Fab (Fab fragment)

Three septic animals were treated with cH36-Fab look for any differences
5   between use of whole antibody and Fab fragment. Treatment protocols generally
followed procedures already discussed above. Although the group was too small for
detailed statistical analyses, the data suggested that the Fab fragment had effect in
attenuating sepsis-induced activation of coagulation, with increased TAT values and
depletion of fibrinogen similar to septic controls.   However, that effect was less
10   pronounced then results achieved with whole antibody. Correspondingly, there was
less consistent improvement in gas exchange (AaDO2), pulmonary hypertension
(PAM), and lung compliance (Cst) than in animals treated with whole cH36 antibody.
Biochemically, lung MPO values were similar to septic controls. Without wishing to
be bound to theory, the difference in effect between cH36 and its Fab fragment may
15   be due to the lower affinity of the Fab fragment for TF in the animal model.

EXAMPLE 9: Anti-Tissue Factor Inhibition of Collagen-Induced Arthritis in
20   Transgenic Mice Expressing Human Tissue Factor

Collagen-induced arthritis (CIA) is an established experimental model of
rheumatoid arthritis which is induced in susceptible strains of mice following
immunization with type II collagen. In addition to the immune mediated mechanism
25   in the pathogenesis of rheumatoid arthritis, tissue factor initiated activation of the
coagulation cascade has also been implicated in the progression of the disease. Fibrin
deposition in the affected joints resulting from the activation of coagulation is
believed to contribute to synovial thickening and joint inflammation. To determine
whether treatment with anti-tissue factor antibodies will prevent development of
30   rheumatoid arthritis mice will be injected with cH36.

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To induce CIA 7-12 week old mice are injected intradermally at the base of
the tail with 100μg of type II collagen emulsified in Complete Freund's Adjuvant and
given a boost injection with 100 μg of type II collagen emulsified in Incomplete
Freund's Adjuvant at day 21. Immediately prior to the boost injection mice are given

5   0.3 mg anti-tissue factor antibody by IV injection (the control group are injected with
PBS). Anti-tissue factor antibody injections (0.3 mg) are subsequently given weekly
for the duration of the study (the control group are injected with PBS).

Animals are assessed for redness and swelling of the limbs and a clinical
10   score is allocated three times per week. The clinical severity is scored as follows: 1
point for each swollen digit except the thumb (maximum 4), 1 Point for the tarsal or
carpal joint, and one point for the metatarsal or metacarpal joint with a maximum
score of 6 for a hindpaw and 5 for a forepaw. Each paw is graded individually, the
cumulative clinical arthritic score per mouse can reach a maximum of 22 points.

15

The present provisional application has information relating to published U.S.
patent application no. 20030190705 which application is related to U.S Application
No. 09/990,586 as filed on November 21, 2001, which application claims priority to
U.S. Provisional Application USSN 60/343,306 as filed on October 29, 2001. The

20   U.S Application No. 09/990,586 is related to U.S. Application No. 09/293,854 (now
U.S. Pat. No. 6,555,319) which application is a divisional of U.S. Application No.
08/814,806 (now U.S. Pat. No. 5,986,065) and the U.S. Application No. 10/230,880
claims priority to U.S Application No. 09/990,586. The disclosures of the U.S.
Application Nos. 10/230,880, 09/990,586, 60/343,306 and U.S. Pat. Nos. 5,986,065

25   and 6,555,319 are each incorporated by reference. Also incorporated by reference is
the disclosure of published U.S. patent application no. 20030190705.

The present provisional application is further related to U.S. provisional
application Serial No. 60/480,254 as filed on June 19, 2003, the disclosure of which
30   is incorporated by reference.

The invention has been described in detail with reference to preferred embodiments thereof. However, it will be appreciated that those skilled in the art, upon consideration of the disclosure, may make modification and improvements within the spirit and scope of the invention. All references disclosed herein are incorporated herein by reference.

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What is claimed is:

1.   A method for preventing or treating a sepsis or inflammatory disease in a
mammal, the method comprising administering to the mammal a therapeutically

5   effective amount of at least one humanized antibody, chimeric antibody, or fragment
thereof that binds specifically to tissue factor (TF) to form a complex, wherein factor
X or factor IX binding to the complex is inhibited and the administration is sufficient
to prevent or treat the sepsis in the mammal.

10   2.   The method of claim 1, wherein the humanized antibody, chimeric antibody
or the fragment exhibits at least one of: 1) a dissociation constant (K_d) for the TF of
less than about 0.5 nM; or 2) an affinity constant (K_a) for the TF of less than about 10
x 10^{10} M^{-1}.

15   3.   The method of claims 1-2, wherein the humanized antibody, chimeric
antibody or fragment thereof is further characterized by having a binding specificity
for the TF about equal or greater than the antibody obtained from cell line H36.D2.B7
deposited under ATCC Accession No. HB-12255.

20   4.   The method of claims 1-3, wherein the humanized antibody, chimeric
antibody or fragment thereof is further characterized in that factor X or factor IX
activation by the TF-factor VIIa complex is blocked.

5.   The method of claims 1-4, wherein administration of the humanized antibody,
25   chimeric antibody or fragment to the mammal increases survival time by at least
about 2-fold as determined by a standard *in vivo* septic shock assay.

6.   The method of claims 1-5, wherein administration of the humanized antibody,
chimeric antibody or fragment to the mammal attenuates at least one of inflammatory
30   cytokine (interleukin-6 (IL-6) and interleukin-8 (IL-8), interleukin-1beta (IL-1β),

tumor necrosis factor-alpha (TNFα) or tumor necrosis factor receptor (TNFR)) levels
in the mammal after at least about 5 hours.

7.   The method of claims 1-6, wherein about 5 minutes after administration of the
humanized antibody, chimeric antibody or fragment, the mammal exhibits a blood
clotting time of between from about 30 to about 350 seconds as determined by a
standard prothrombin time assay.

8.   The method of claims 1-7, wherein the amount of the administered humanized
antibody, chimeric antibody, or fragment is sufficient to inhibit platelet deposition by
at least about 50% as determined by a standard platelet deposition assay.

9.   The method of claims 1-8, wherein the humanized antibody has an IgG1 or
IgG4 isotype.

10.   The method of claims 1-9, wherein the human TF binding fragment is Fab,
Fab', or F(ab)$_2$.

11.   The method of claims 1-10, wherein the humanized antibody is a monoclonal
antibody.

12.   The method of claims 1-10, wherein the humanized antibody or fragment
thereof is a single-chain.

13.   The method of claims 1-28, wherein the mammal is a primate.

14.   The method of claim 13, wherein the primate is a human patient.

15.   The method of claims 1-14, wherein the sepsis is associated with at least one
of disseminated intravascular coagulation (DIC), fibrin deposition, thrombosis, and
lung injury.

16.   The method of claims 1-14, wherein the inflammatory disease is associated with at least one of arthritis, preferably rheumatoid arthritis, glomerulonephritis, multiple sclerosis, psoriasis, Sjogren's syndrome and inflammatory bowel disease.

17.   The method of claims 1-28, wherein the amount of the humanized antibody, chimeric antibody or fragment administered to the mammal is between about 0.01 to about 25 (mg/kg).

18.   A kit for performing the method of claims 1-16, wherein the kit includes at least one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to human TF to form a complex, wherein factor X or factor IX binding to the complex is inhibited.

19.   The kit of claim 17, wherein the humanized antibody, chimeric antibody, or fragment thereof is provided in a pharmaceutically acceptable vehicle.

20.   The kit of claims 17-18, wherein the humanized antibody, chimeric antibody, or fragment thereof is lyophilized and the kit further includes a pharmaceutically acceptable vehicle for dissolving the humanized antibody, chimeric antibody or fragment.

21.   A method for reducing an inflammatory cytokine production in a mammal, the method comprising administering to the mammal a therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to TF to form a complex, wherein factor X or factor IX binding to the complex is inhibited and the administration is sufficient to reduce the inflammatory cytokine production in the mammal.

22.   The method of claim 21, wherein the inflammatory cytokine is at least one of inflammatory cytokine (interleukin-6 (IL-6) and interleukin-8 (IL-8), interleukin-

1beta (IL-1β), tumor necrosis factor-alpha (TNFα) or tumor necrosis factor receptor (TNFR)).

23.   The method of claims 21-22, wherein the administered antibody, chimeric
5   antibody or fragment there of is encompassed by any one of claims 2-12.

22.   A method for preventing or treating a sepsis-related condition in a mammal, the method comprising administering to the mammal a therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment thereof
10   that binds specifically to tissue factor (TF) to form a complex, wherein factor X or factor IX binding to the complex is inhibited and the administration is sufficient to prevent or treat the condition in the mammal.

23.   The method of claim 22, wherein the sepsis-related condition is one or more
15   of disseminated intravascular coagulation (DIC), fibrin deposition, thrombosis,lung injury, or sepsis-associated renal disorder .

24.   The method of claim 23, wherein the lung injury is acute lung injury (ALI), or acute respiratory distress syndrome (ARDS).
20
25.   The method of claim 23, wherein the sepsis-associated renal disorder is acute tubular necrosis (ACN).

26.   The method of claims 22-25, wherein the administered antibody, chimeric
25   antibody or fragment there of is encompassed by any one of claims 2-12.

27.   A method for preventing or treating sepsis-induced anemia in a mammal, the method comprising administering to the mammal a therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment thereof that binds
30   specifically to tissue factor (TF) to form a complex, wherein factor X or factor IX

binding to the complex is inhibited and the administration is sufficient to prevent or treat the condition in the mammal.

28.   The method of claim 27, wherein the administered antibody, chimeric antibody or fragment there of is encompassed by any one of claims 2-12.

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FIG. 2

pSUN34
11328 bp

Bam H I (1)
Nhe I (16)
SV40 PROMOTER
Neomycin Resistance
SV40 POLY A
pUC 19 backbone
Ampicillin Resistance
Pvu I (3647)
Spe I (4449)
CMV PROMOTER/ENHANCER
Hind III (5091)
Age I (5181)
LC variable
Bst BI (5522)

BGH polyA
Human IgG1HC
Age I (10154)
EcoR 1 (10044)
HC variable
Hpa I (9617)
Hind III (9609)
CMV PROMOTER/ENHANCER
Spe I (8967)
BGH POLY A
Bsm BI (8457)
Xho I (8454)
Bsm BI (8389)
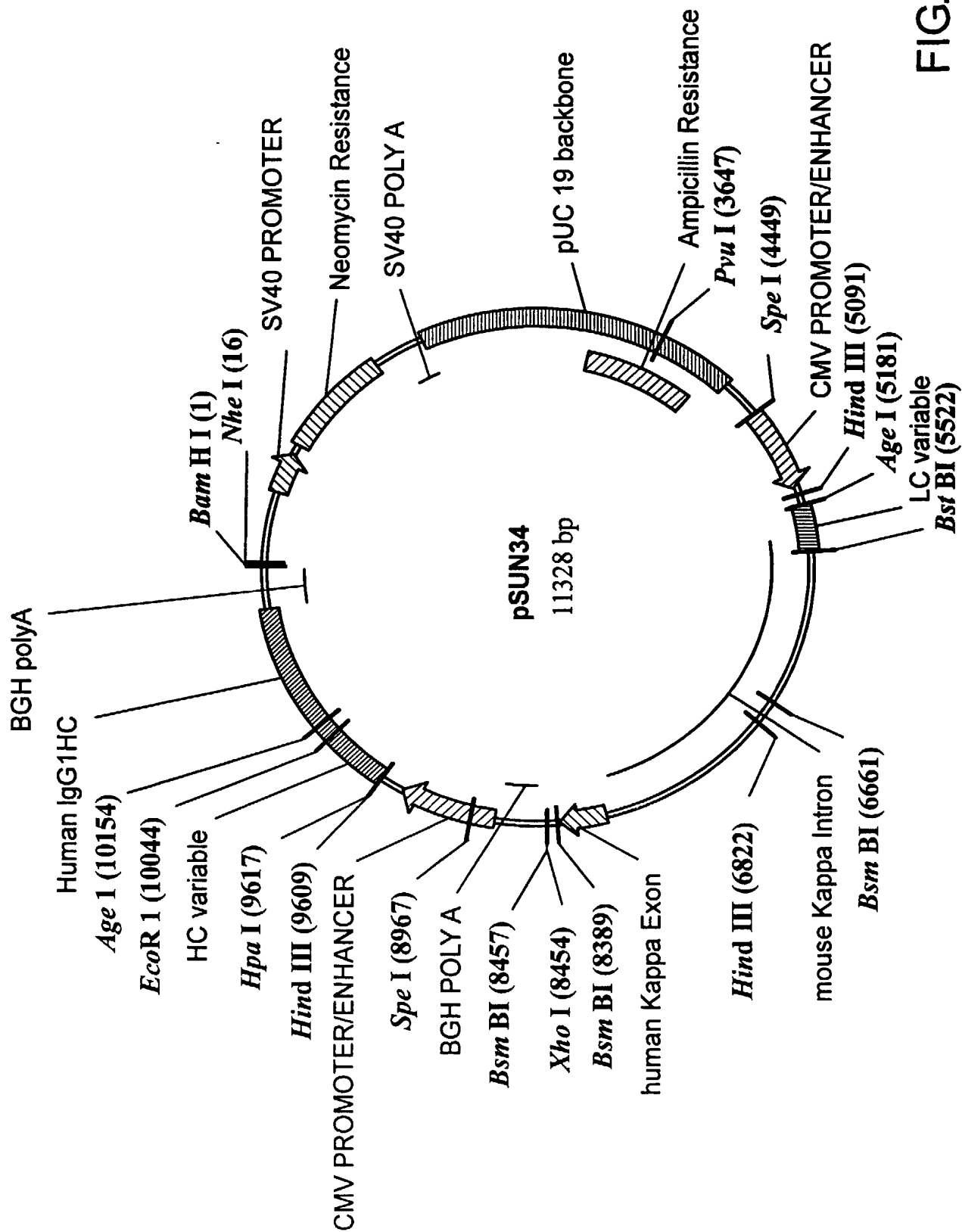human Kappa Exon
Hind III (6822)
mouse Kappa Intron
Bsm BI (6661)

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Exept for HC-08, all others HC mutants and cH36 contain F at position 64 in CDR2.
HC-08 has the mutation F64 to L (change from F to L at position 64)

```
FR1 (30 AA)                        FR2 (14 AA)     FR3 (32 AA)                       FR4 (11 AA)   Names
1        10        20    30 36     49 67           75       85       95  107    117
EIQLQQSGPELVKPGASVQVSCKTSGYSFT  WVRQSHGKSLEWIG  KATLTVDKSSTTAFMHLNSLTSDDSAVYFCAR  WGQGTTLTVSS  CH36-HC
QIQLQQSGPELVKPGASVQVSCKTSGYSFT  WVRQSHGKSLEWIG  KATLTVDKSSTTAFMHLNSLTSDDSAVYFCAR  WGQGTTVTVSS  HC-01
QIQLQQSGPELVKPGASVQVSCKTSGYSFT  WVRQSPGKSLEWIG  KATLTVDKSSTTAFMHLNSLTSDDSAVYFCAR  WGQGTTVTVSS  HC-02
QIQLQQSGPELVKPGASVQVSCKTSGYSFT  WVRQSPGKGLEWIG  KATLTVDKSSTTAFMHLNSLRSEDTAVYFCAR  WGQGTTVTVSS  HC-03
QIQLQQSGPELVKPGASVQVSCKTSGYSFT  WVRQSPGKGLEWIG  KATLTVDKSSTTAFMELSSLRSEDTAVYFCAR  WGQGTTVTVSS  HC-04
QIQLQQSGPELVKPGASVQVSCKTSGYSFT  WVRQSPGKGLEWIG  KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR  WGQGTTVTVSS  HC-05
DMQLQQSGGELVKPGASVRVSCKASGYSFT  WVRQSPGKGLEWIG  KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR  WGQGTTVTVSS  HC-06
QIQLVQSGGELVKPGASVRVSCKASGYSFT  WVRQSPGKGLEWIG  KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR  WGQGTTVTVSS  HC-07
QIQLVQSGGEVKKPGASVRVSCKASGYSFT  WVRQSPGKGLEWIG  KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR  WGQGTTVTVSS  HC-08
QIQLVQSGGEVKKPGASVRVSCKASGYSFT  WVRQSPGKGLEWIG  KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR  WGQGTTVTVSS  HC-08R1
QIQLVQSGPEVKRPGASVRVSCKASGYSFT  WVRQSPGKGLEWIG  KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR  WGQGTTVTVSS  HC-11
QIQLVQSGPELKKPGASVRVSCKASGYSFT  WVRQSPGKGLEWIG  KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR  WGQGTTVTVSS  HC-12
QIQLVQSGPELVKPGASVRVSCKASGYSFT  WVRQSPGKGLEWIG  KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR  WGQGTTVTVSS  HC-09
QIQLVQSGPEVVKPGASVRVSCKASGYSFT  WVRQSPGKGLEWIG  KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR  WGQGTTVTVSS  HC-10
```

FIG. 4A

Heavy Chain CDR Sequences

```
CDR1 (5aa)
31    35
DYNVY
DYNVY
```

FIG. 4B

```
CDR2 (17 AA)
50                   66
YIDPYNGITIYDQNFKG
YIDPYNGITIYDQNLKG
```

FIG. 4C

```
CDR3 (8AA)          Names
99      106
DVTTALDF            cH36
DVTTALDF            HC-08
```

FIG. 4D

Sequence of human kappa Light Chain Constant Domain:

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKH

KVYACEVTHQGLSSPVTKSFNRGEC

FIG. 5A

Sequence of human IgG1 Heavy Chain Constant Domain:

EFASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC

NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV

HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL

VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Notes: 1. Amino acid sequence in one letter code.
2. Immediately following the last residue of the framework 4 (FR4) variable domain is the first residue of the constant domain for hOAT or hFAT.
3. LC constant are the same for hOAT and hFAT.

FIG. 5B

Sequence of human kappa Light Chain Constant Domain:

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEK

30 HKVYACEVTHQGLSSPVTKSFNRGEC

FIG. 6A

Sequence of human IgG4 Heavy Chain Constant Domain:

EFASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY

5 TCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGV

EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSL

10 TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

Notes: 1. Amino acid sequence in one letter code.
2. Immediately following the last residue of the framework 4 (FR4) variable domain is the first residue of the constant domain for hOAT or hFAT.
3. LC constant domain is the same for hOAT and hFAT.

FIG. 6B

FIG. 7A

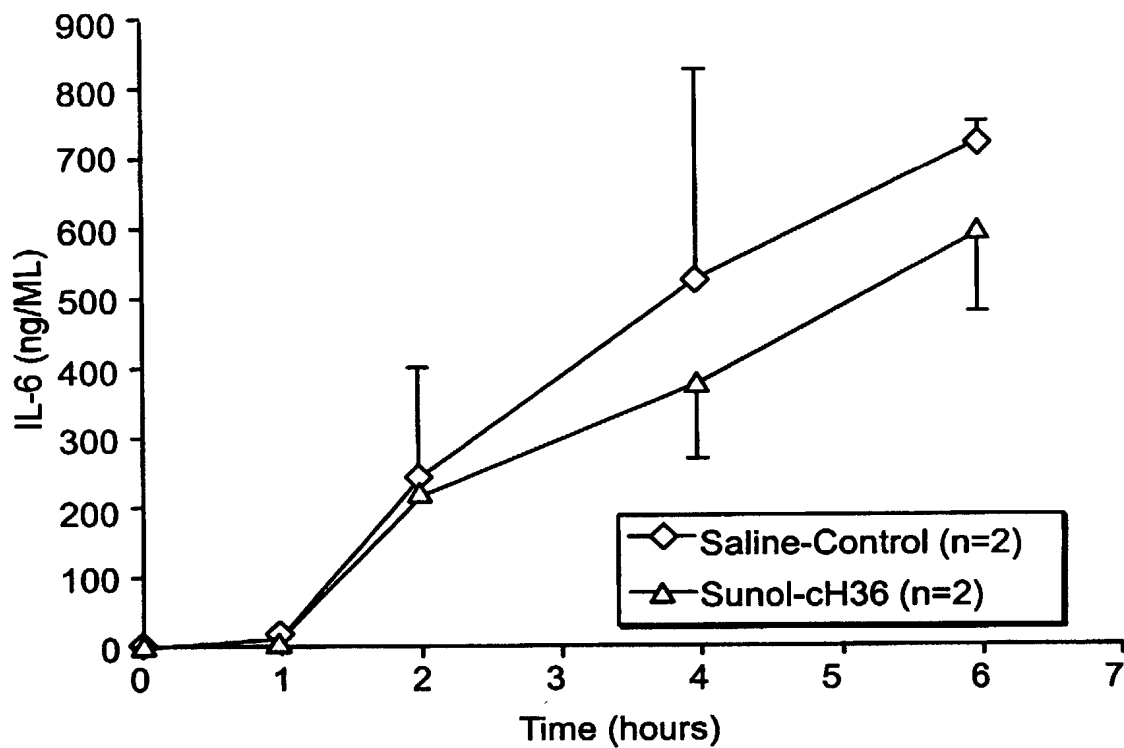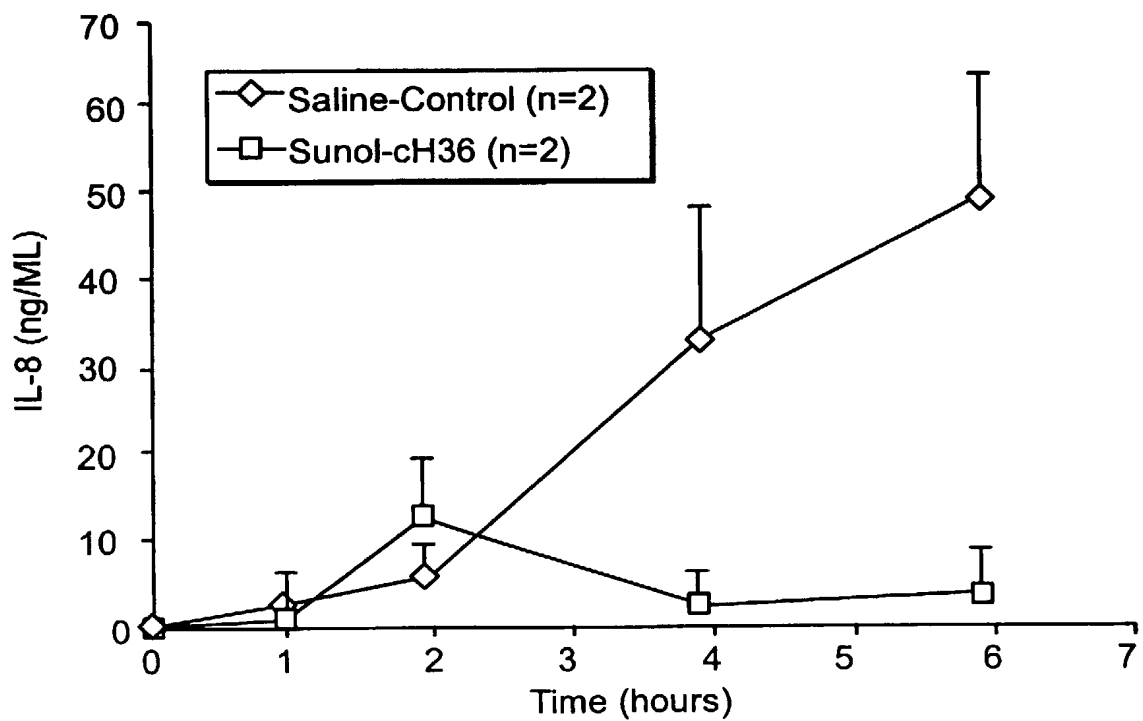FIG. 7B

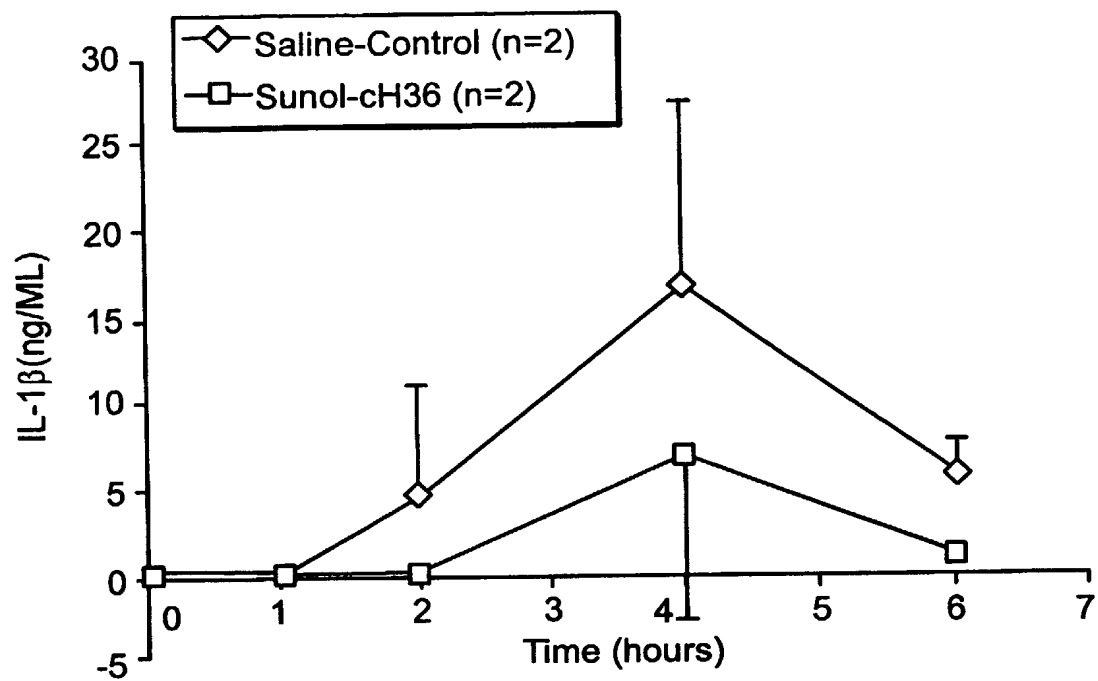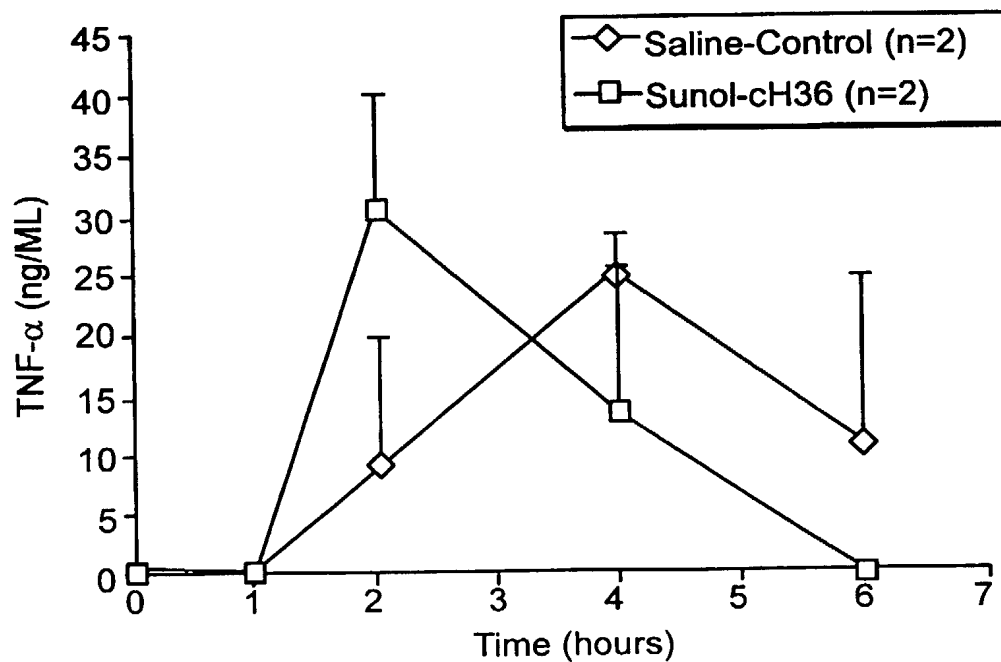FIG. 7C

FIG. 7D

AaDO$_2$

FIG. 8A

PAM

FIG. 8B

FIG. 8C

FIG. 9A

FIG. 9B

FIG. 10A

PT

FIG. 10B

PTT

FIG. 10C

FIG. 10D

FIG. 11A

FIG. 11B

FIG. 12

Mean Urine Output

FIG. 13A

Mean Blood pH
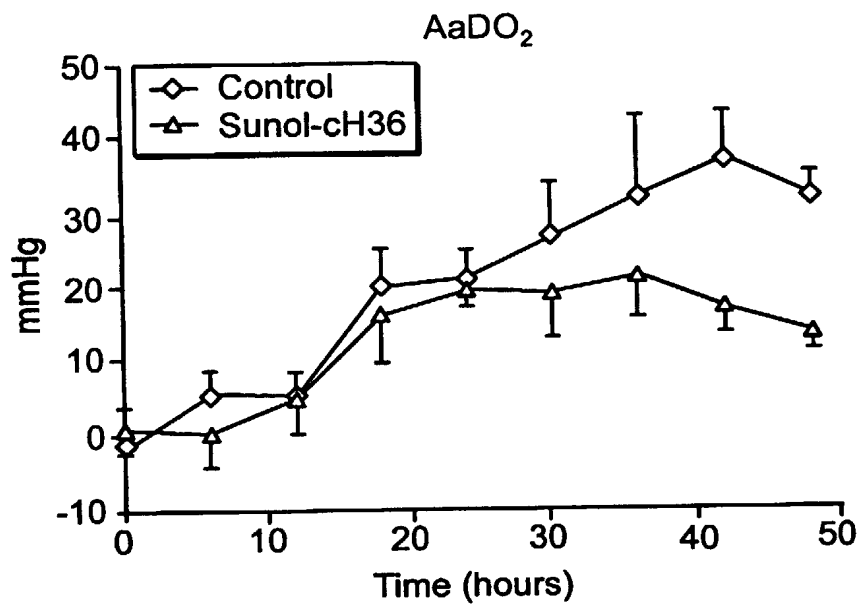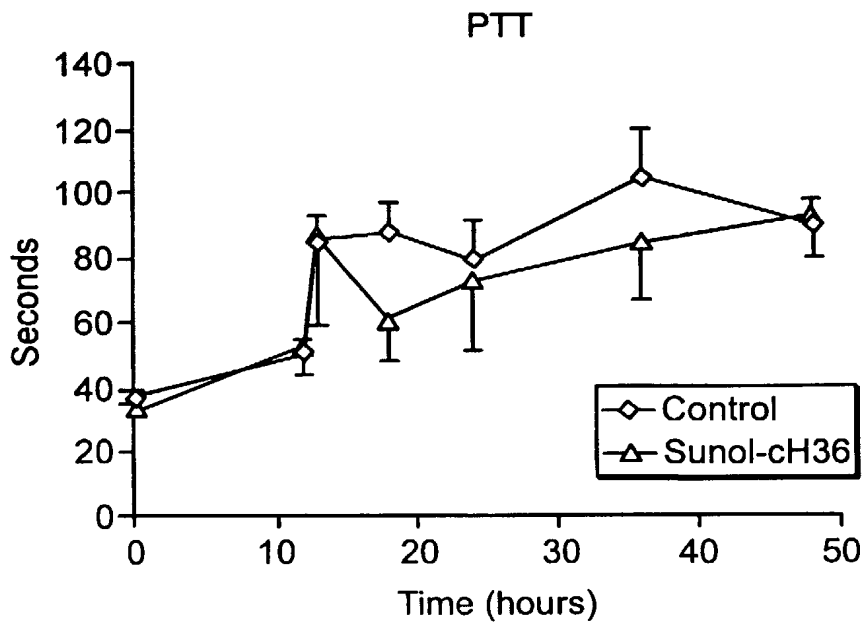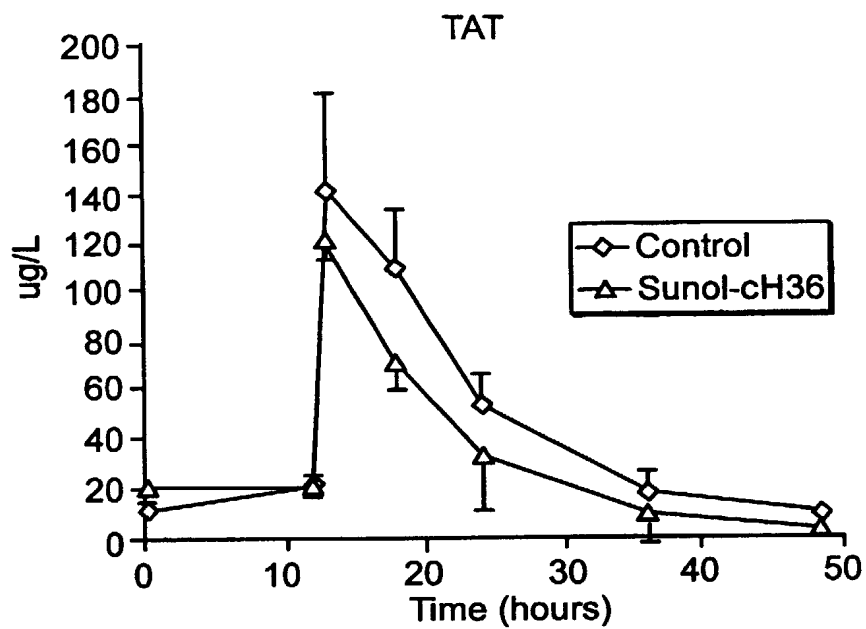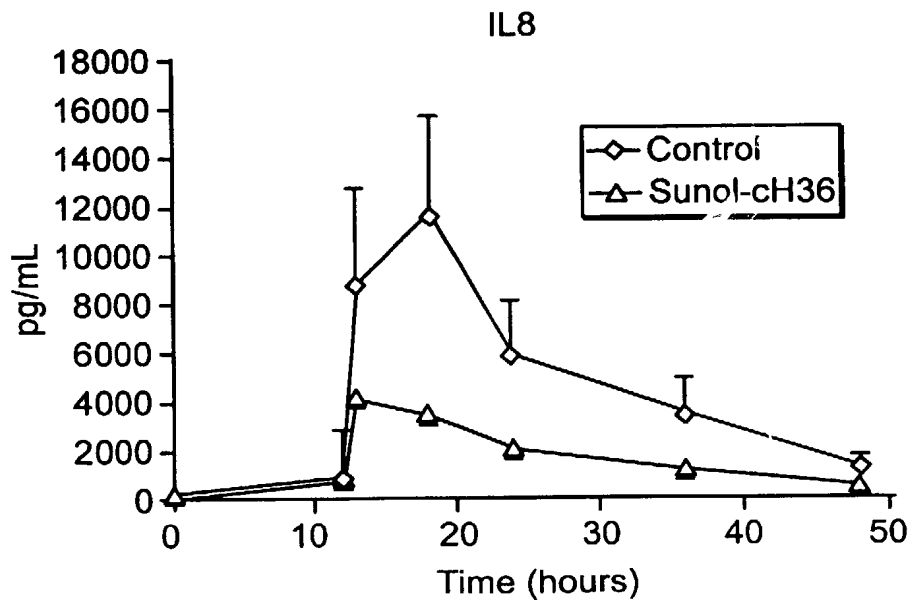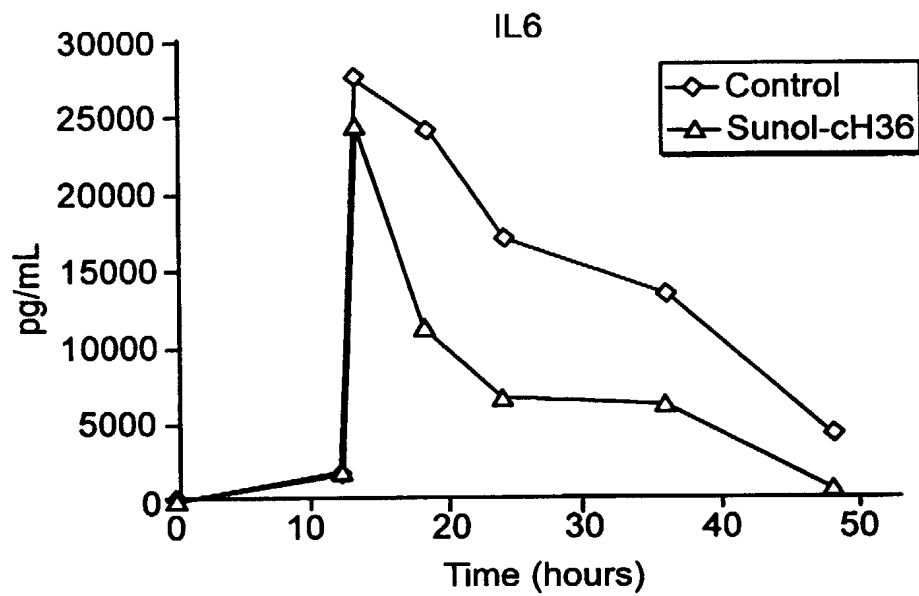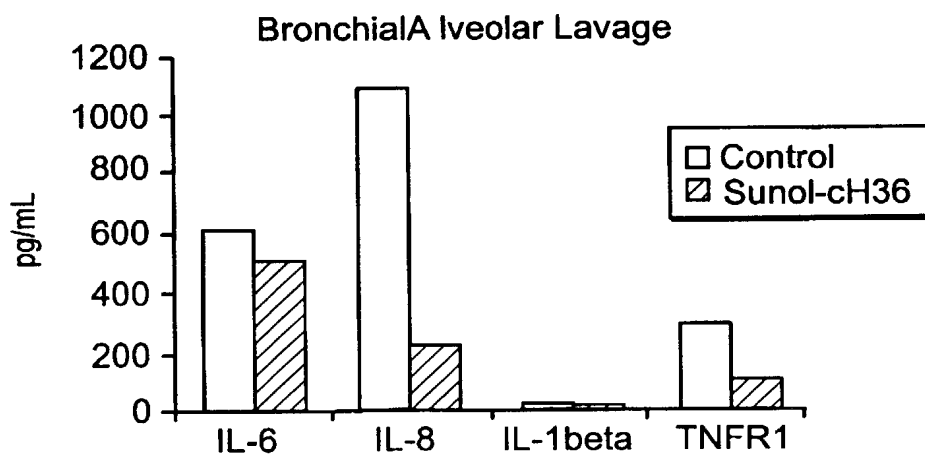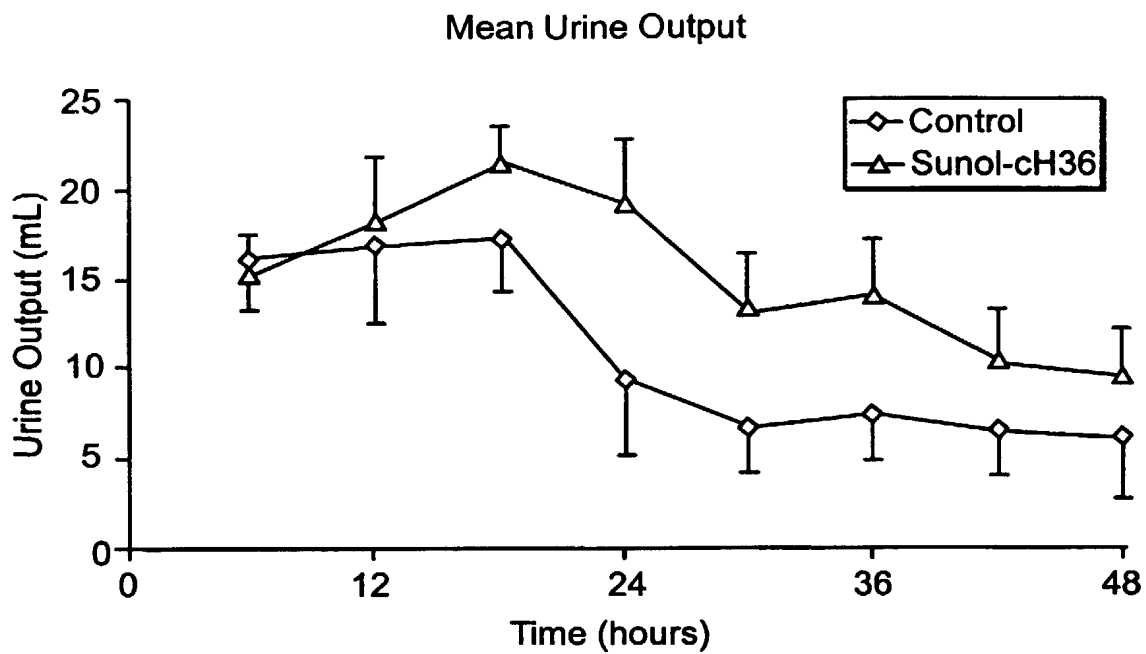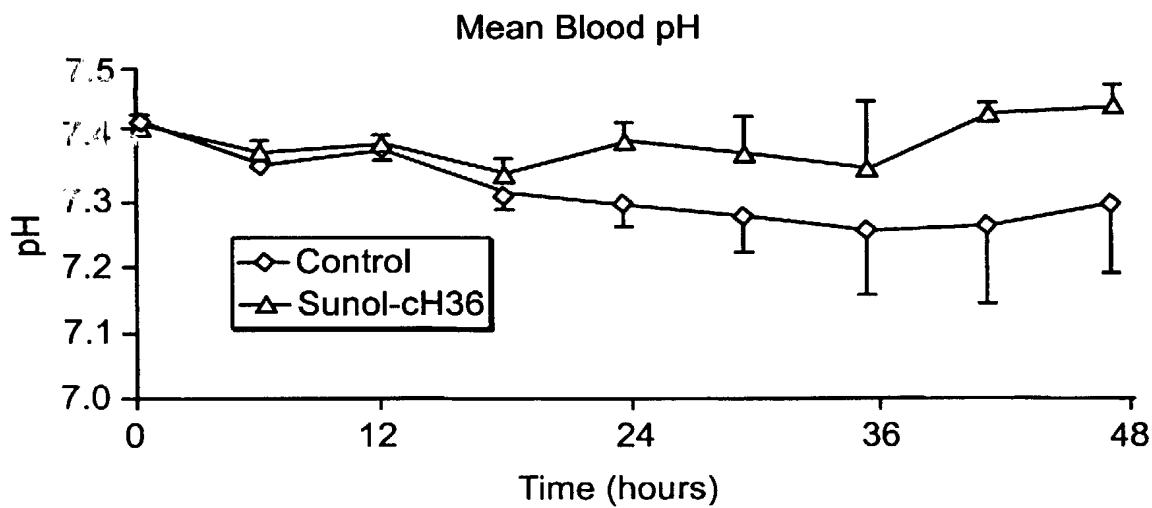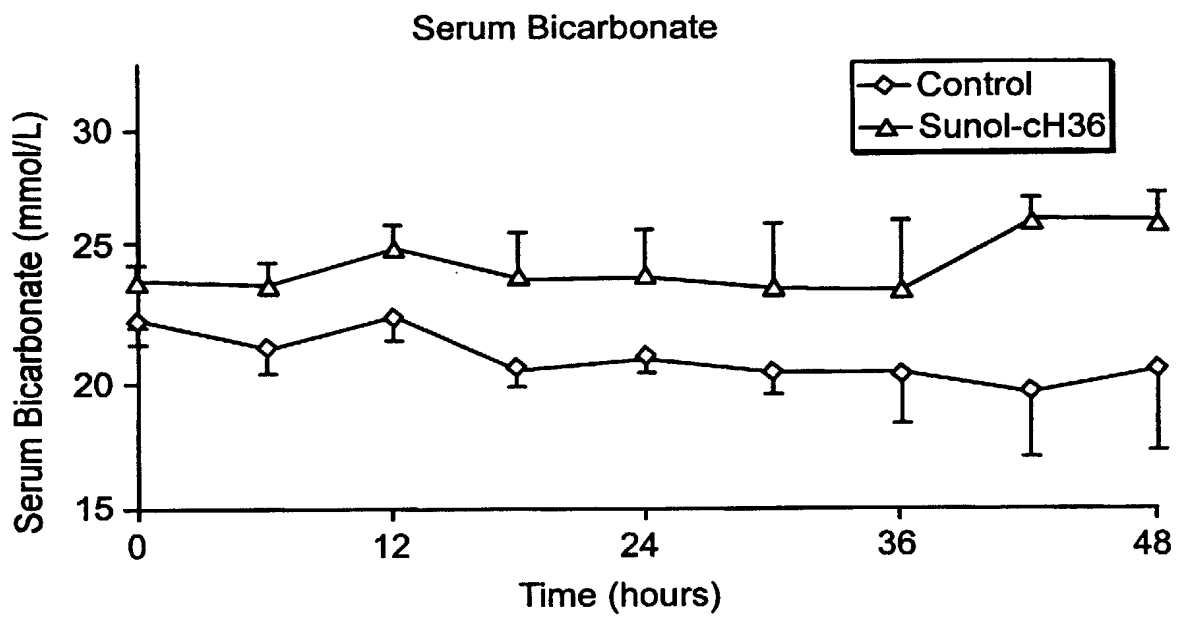
FIG. 13B

FIG. 13C

SEQUENCE LISTING

(1) GENERAL INFORMATION

5

(i) APPLICANT:

(ii) TITLE OF THE INVENTION:

10   (iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:
  (A) ADDRESSEE:
  (B) STREET:
15   (C) CITY:
  (D) STATE:
  (E) COUNTRY:
  (F) ZIP:

20   (v) COMPUTER READABLE FORM:
  (A) MEDIUM TYPE: Diskette
  (B) COMPUTER: IBM Compatible
  (C) OPERATING SYSTEM: DOS
  (D) SOFTWARE: FastSEQ Version 1.5
25

(vi) CURRENT APPLICATION DATA:
  (A) APPLICATION NUMBER:
  (B) FILING DATE:
  (C) CLASSIFICATION:
30

(vii) PRIOR APPLICATION DATA:
  (A) APPLICATION NUMBER:
  (B) FILING DATE:

35   (viii) ATTORNEY/AGENT INFORMATION:
  (A) NAME:
  (B) REGISTRATION NUMBER:
  (C) REFERENCE/DOCKET NUMBER:

40   (ix) TELECOMMUNICATION INFORMATION:
  (A) TELEPHONE:
  (B) TELEFAX:
  (C) TELEX:

45   (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 321 base pairs
  (B) TYPE: nucleic acid
50   (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
55   (iv) ANTISENSE: NO

(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GACATTCAGA TGACCCAGTC TCCTGCCTCC CAGTCTGCAT CTCTGGGAGA AAGTGTCACC
60
ATCACATGCC TGGCAAGTCA GACCATTGAT ACATGGTTAG CATGGTATCA GCAGAAACCA
120
GGGAAATCTC CTCAGCTCCT GATTTATGCT GCCACCAACT TGGCAGATGG GGTCCCATCA
180
AGGTTCAGTG GCAGTGGATC TGGCACAAAA TTTTCTTTCA AGATCAGCAG CCTACAGGCT
240
GAAGATTTTG TAAATTATTA CTGTCAACAA GTTTACAGTT CTCCATTCAC GTTCGGTGCT
300
GGGACCAAGC TGGAGCTGAA A
321

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE: N-terminal
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Gln Ser Ala Ser Leu Gly
1             5                   10                  15
Glu Ser Val Thr Ile Thr Cys Leu Ala Ser Gln Thr Ile Asp Thr Trp
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Gln Leu Leu Ile
            35                  40                  45
Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Lys Phe Ser Phe Lys Ile Ser Ser Leu Gln Ala
65                  70                  75                  80
Glu Asp Phe Val Asn Tyr Tyr Cys Gln Gln Val Tyr Ser Ser Pro Phe
                85                  90                  95
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

           (iii) HYPOTHETICAL: NO
           (iv) ANTISENSE: NO
           (v) FRAGMENT TYPE:
           (vi) ORIGINAL SOURCE:
5
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

     GAGATCCAGC TGCAGCAGTC TGGACCTGAG CTGGTGAAGC CTGGGGCTTC AGTGCAGGTA
     60
10   TCCTGCAAGA CTTCTGGTTA CTCATTCACT GACTACAACG TGTACTGGGT GAGGCAGAGC
     120
     CATGGAAAGA GCCTTGAGTG GATTGGATAT ATTGATCCTT ACAATGGTAT TACTATCTAC
     180
     GACCAGAACT TCAAGGGCAA GGCCACATTG ACTGTTGACA AGTCTTCCAC CACAGCCTTC
15   240
     ATGCATCTCA ACAGCCTGAC ATCTGACGAC TCTGCAGTTT ATTTCTGTGC AAGAGATGTG
     300
     ACTACGGCCC TTGACTTCTG GGGCCAAGGC ACCACTCTCA CAGTCTCCTC A
     351
20
           (2) INFORMATION FOR SEQ ID NO:4:

           (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 117 amino acids
25   (B) TYPE: amino acid
               (C) STRANDEDNESS: single
               (D) TOPOLOGY: linear

           (ii) MOLECULE TYPE: peptide
30   (iii) HYPOTHETICAL: NO
           (iv) ANTISENSE: NO
           (v) FRAGMENT TYPE: N-terminal
           (vi) ORIGINAL SOURCE:

35   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

     Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
     1   5   10   15
     Ser Val Gln Val Ser Cys Lys Thr Xaa Gly Tyr Ser Phe Thr Asp Tyr
40   20   25   30
     Asn Val Tyr Trp Val Arg Gln Ser His Gly Lys Ser Leu Glu Trp Ile
            35   40   45
     Gly Tyr Ile Asp Pro Tyr Asn Gly Ile Thr Ile Tyr Asp Gln Asn Phe
            50   55   60
45   Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Phe
     65   70   75   80
     Met His Leu Asn Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys
                        85   90   95
     Ala Arg Asp Val Thr Thr Ala Leu Asp Phe Trp Gly Gln Gly Thr Thr
50   100   105   110
     Leu Thr Val Ser Ser
            115

           (2) INFORMATION FOR SEQ ID NO:5:
55
           (i) SEQUENCE CHARACTERISTICS:

                        (A) LENGTH: 7 amino acids
                        (B) TYPE: amino acid
                        (C) STRANDEDNESS: single
                        (D) TOPOLOGY: linear

  5
                     (ii) MOLECULE TYPE: peptide
                     (iii) HYPOTHETICAL: NO
                     (iv) ANTISENSE: NO
                     (v) FRAGMENT TYPE: N-terminal
 10   (vi) ORIGINAL SOURCE:

                     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

      Leu Ala Ser Gln Thr Ile Asp
 15   1   5

                        (2) INFORMATION FOR SEQ ID NO:6:

                     (i) SEQUENCE CHARACTERISTICS:
 20   (A) LENGTH: 7 amino acids
                        (B) TYPE: amino acid
                        (C) STRANDEDNESS: single
                        (D) TOPOLOGY: linear

 25   (ii) MOLECULE TYPE: peptide
                     (iii) HYPOTHETICAL: NO
                     (iv) ANTISENSE: NO
                     (v) FRAGMENT TYPE: N-terminal
                     (vi) ORIGINAL SOURCE:
 30   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

      Ala Ala Thr Asn Leu Ala Asp
       1   5   .

 35   (2) INFORMATION FOR SEQ ID NO:7:

                     (i) SEQUENCE CHARACTERISTICS:
                        (A) LENGTH: 9 amino acids
                        (B) TYPE: amino acid
 40   (C) STRANDEDNESS: single
                        (D) TOPOLOGY: linear

                     (ii) MOLECULE TYPE: peptide
                     (iii) HYPOTHETICAL: NO
 45   (iv) ANTISENSE: NO
                     (v) FRAGMENT TYPE: N-terminal
                     (vi) ORIGINAL SOURCE:

                     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
 50
      Gln Gln Val Tyr Ser Ser Pro Phe Thr
       1   5

                        (2) INFORMATION FOR SEQ ID NO:8:
 55
                     (i) SEQUENCE CHARACTERISTICS:

```
              (A) LENGTH: 6 amino acids
              (B) TYPE: amino acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
 5
          (ii) MOLECULE TYPE: peptide
          (iii) HYPOTHETICAL: NO
          (iv) ANTISENSE: NO
          (v) FRAGMENT TYPE: N-terminal
10        (vi) ORIGINAL SOURCE:

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

     Thr Asp Tyr Asn Val Tyr
15    1               5

              (2) INFORMATION FOR SEQ ID NO:9:

          (i) SEQUENCE CHARACTERISTICS:
20            (A) LENGTH: 17 amino acids
              (B) TYPE: amino acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

25        (ii) MOLECULE TYPE: peptide
          (iii) HYPOTHETICAL: NO
          (iv) ANTISENSE: NO
          (v) FRAGMENT TYPE: N-terminal
          (vi) ORIGINAL SOURCE:
30
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

     Tyr Ile Asp Pro Tyr Asn Gly Ile Thr Ile Tyr Asp Gln Asn Phe Lys
      1               5                  10                  15
35   Gly

              (2) INFORMATION FOR SEQ ID NO:10:

          (i) SEQUENCE CHARACTERISTICS:
40            (A) LENGTH: 8 amino acids
              (B) TYPE: amino acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

45        (ii) MOLECULE TYPE: peptide
          (iii) HYPOTHETICAL: NO
          (iv) ANTISENSE: NO
          (v) FRAGMENT TYPE: N-terminal
          (vi) ORIGINAL SOURCE:
50
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

     Asp Val Thr Thr Ala Leu Asp Phe
      1               5
55
              (2) INFORMATION FOR SEQ ID NO:11:
```

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 21 base pairs
          (B) TYPE: nucleic acid
    5   (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA
        (iii) HYPOTHETICAL: NO
    10 (iv) ANTISENSE: NO
        (v) FRAGMENT TYPE:
        (vi) ORIGINAL SOURCE:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
    15
    CTGGCAAGTC AGACCATTGA T
        21

            (2) INFORMATION FOR SEQ ID NO:12:
    20
        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 21 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
    25   (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA
        (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
    30 (v) FRAGMENT TYPE:
        (vi) ORIGINAL SOURCE:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

    35 GCTGCCACCA ACTTGGCAGA T
        21

            (2) INFORMATION FOR SEQ ID NO:13:

    40 (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 28 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    45
        (ii) MOLECULE TYPE: DNA
        (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
        (v) FRAGMENT TYPE:
    50 (vi) ORIGINAL SOURCE:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

    CAACAAGTTT ACAGTTCTCC ATTCACGT
    55 28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 18 base pairs
5   (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA
10 (iii) HYPOTHETICAL: NO
    (iv) ANTISENSE: NO
    (v) FRAGMENT TYPE:
    (vi) ORIGINAL SOURCE:

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACTGACTACA ACGTGTAC
18
        (2) INFORMATION FOR SEQ ID NO:15:
20
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 51 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
25   (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA
    (iii) HYPOTHETICAL: NO
    (iv) ANTISENSE: NO
30 (v) FRAGMENT TYPE:
    (vi) ORIGINAL SOURCE:

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

35 TATATTGATC CTTACAATGG TATTACTATC TACGACCAGA ACTTCAAGGG C
51

        (2) INFORMATION FOR SEQ ID NO:16:

40 (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
45
    (ii) MOLECULE TYPE: cDNA
    (iii) HYPOTHETICAL: NO
    (iv) ANTISENSE: NO
    (v) FRAGMENT TYPE:
50 (vi) ORIGINAL SOURCE:

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATGTGACTA CGGCCCTTGA CTTC
55 24
        (2) INFORMATION FOR SEQ ID NO:17:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 23 base pairs
           (B) TYPE: nucleic acid
5   (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA
        (iii) HYPOTHETICAL: NO
10   (iv) ANTISENSE: NO
        (v) FRAGMENT TYPE:
        (vi) ORIGINAL SOURCE:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
15
   GCACCTCCAG ATGTTAACTG CTC
        23

              (2) INFORMATION FOR SEQ ID NO:18:
20
        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 20 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
25   (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA
        (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
30   (v) FRAGMENT TYPE:
        (vi) ORIGINAL SOURCE:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
   GAARTAVCCC TTGACCAGGC
35   20

              (2) INFORMATION FOR SEQ ID NO:19:

        (i) SEQUENCE CHARACTERISTICS:
40   (A) LENGTH: 35 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

45   (ii) MOLECULE TYPE: DNA
        (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
        (v) FRAGMENT TYPE:
        (vi) ORIGINAL SOURCE:
50
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

   GGAGGCGGCG GTTCTGACAT TGTGMTGWCM CARTC
        35
55
              (2) INFORMATION FOR SEQ ID NO:20:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 45 base pairs
           (B) TYPE: nucleic acid
5   (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA
        (iii) HYPOTHETICAL: NO
10   (iv) ANTISENSE: NO
        (v) FRAGMENT TYPE:
        (vi) ORIGINAL SOURCE:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
15

    ATTTCAGGCC CAGCCGGCCA TGGCCGARGT YCARCTKCAR CARYC
    45

            (2) INFORMATION FOR SEQ ID NO:21:
20

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 33 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
25   (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA
        (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
30   (v) FRAGMENT TYPE:
        (vi) ORIGINAL SOURCE:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

35 CCCGGGCCAC CATGKCCCCW RCTCAGYTYC TKG
    33

            (2) INFORMATION FOR SEQ ID NO:22:

40   (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 35 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
45
        (ii) MOLECULE TYPE: DNA
        (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
        (v) FRAGMENT TYPE:
50   (vi) ORIGINAL SOURCE:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

    CCCGGGCCAC CATGGRATGS AGCTGKGTMA TSCTC
55 35

        (2) INFORMATION FOR SEQ ID NO:23:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 52 base pairs
 5   (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA
10   (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
        (v) FRAGMENT TYPE:
        (vi) ORIGINAL SOURCE:

15   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

    ATATACTCGC GACAGCTACA GGTGTCCACT CCGAGATCCA GCTGCAGCAG TC
    52

20   (2) INFORMATION FOR SEQ ID NO:24:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 31 base pairs
           (B) TYPE: nucleic acid
25   (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA
        (iii) HYPOTHETICAL: NO
30   (iv) ANTISENSE: NO
        (v) FRAGMENT TYPE:
        (vi) ORIGINAL SOURCE:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
35
    GACCTGAATT CTAAGGAGAC TGTGAGAGTG G
    31

            (2) INFORMATION FOR SEQ ID NO:25:
40
        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 29 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
45   (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA
        (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
50   (v) FRAGMENT TYPE:
        (vi) ORIGINAL SOURCE:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

55 TTAATTGATA TCCAGATGAC CCAGTCTCC
    29

```
         (2) INFORMATION FOR SEQ ID NO:26:

         (i) SEQUENCE CHARACTERISTICS:
5          (A) LENGTH: 45 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear


10       (ii) MOLECULE TYPE: DNA
         (iii) HYPOTHETICAL: NO
         (iv) ANTISENSE: NO
         (v) FRAGMENT TYPE:
         (vi) ORIGINAL SOURCE:
15
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

    TAATCGTTCG AAAAGTGTAC TTACGTTTCA GCTCCAGCTT GGTCC
    45
20
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(54) Title: COMPOSITIONS AND METHODS FOR TREATING COAGULATION RELATED DISORDERS

(57) Abstract: Disclosed are methods for preventing or treating sepsis, a sepsis-related condition or an inflammatory disease in
a mammal. In one embodiment, the method includes administering to the mammal a therapeutically effective amount of at least
one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to tissue factor (TF) to form a complex in
which factor X or factor IX binding to the complex is inhibited and the administration is sufficient to prevent or treat the sepsis in
the mammal. The invention has a wide spectrum of useful applications including treating sepsis, disorders related to sepsis, and
inflammatory diseases such as arthritis.

5

COMPOSITIONS AND METHODS FOR TREATING
COAGULATION RELATED DISORDERS

10   FIELD OF THE INVENTION

The present invention features compositions and methods for preventing or
treating disorders that relate to undesired activation of blood coagulation. In some
instances, the coagulation contributes to certain inflammatory diseases and related
disorders. In one aspect, the invention provides methods for treating such disorders

15   by administering a therapeutically effective amount of a chimeric or humanized
antibody that binds tissue factor (TF) specifically. The invention has a wide spectrum
of important applications including use in the prevention or treatment of
inflammation including sepsis and arthritis.

20   BACKGROUND OF THE INVENTION

There is increasing recognition of relationship between coagulation and
inflammation. For instance, certain coagulation factors are thought to activate pro-
inflammatory cells and elicit inflammatory responses. On the other hand, some pro-
inflammatory cytokines have been reported to induce TF expression and generate

25   coagulation factors. Studies in certain primates support existence of the relationship
by showing that certain anticoagulants reduce inflammation. See F. B. Taylor Jr. *et
al., J. Clin. Invest.* **79:**918-925 (1987); M. Levi *et al., J. Clin. Invest.* **93:**114-120
(1994); and M. C. Minnema *et al., Blood* **95:**1117-23 (2000).

30   Much has been reported about blood coagulation. For instance, thrombin is a
blood protein that is believed to provide a link between coagulation and
inflammation. Most thrombin is generated by TF-initiation of the coagulation
cascade. Other key coagulation factors include Factor VIIa and Factor Xa.

Thrombin is thought to occupy multiple roles in pro-coagulant, anticoagulant, inflammatory, and mitogenic responses. See generally L. Styer, *Biochemistry*, 3rd Ed., W.H. Freeman Co., New York; and A.G. Gilman *et al.*, in *The Pharmacological Basis of Therapeutics*, 8th Ed., McGraw-Hill Inc., New York.

5

Certain infectious agents are thought to disturb the TF-initiated coagulation cascade. Fortunately, localized activation of the coagulation cascade often keeps the disturbance in check. Sometimes however, aberrant TF expression leads to serious and potentially life-threatening thrombotic disorders. For example, it has been 10 suggested that bacterial induction of TF expression can lead to sepsis, disseminated intravascular coagulation (DIC), widespread fibrin deposition, and other complications. The increase in TF expression is thought to be an important factor in facilitating progression of these disorders. An example of progression of an inflammatory disorder is the progression of acute lung injury (ALI) to acute 15 respiratory distress syndrome (ARDS) followed by progressive injury involving additional organ systems, such as the kidneys, leading to progressively more severe forms of sepsis. See Welty-Wolf, K. *et al. Am. J. Respir. Crit. Care Med.* **164**:1988 (2001), for instance.

20 There have been attempts to understand coagulation related disorders such as sepsis.

For instance, sepsis is a term that has used to characterize a spectrum of clinical conditions facilitated by a host immune response to infection, trauma, or 25 both. Sepsis has been characterized as an uncontrolled cascade of blood coagulation, fibrinolysis, and inflammation. At certain steps in the cascade, an auto-amplification process contributes to an acceleration of coagulation abnormalities, undesired inflammation, and endothelial injury. The amplification process is the result of inflammatory cytokines up-regulating the expression of TF on cells such as 30 endothelial cells and monocytes, resulting in increased activation of the coagulation cascade, which in turn results in the activation of PAR receptors and the up-

regulation of the production of inflammatory cytokines. See Osterud, B. *et al.*, *Thromobsis Hemost.* **83**:861 (2000); Mechtcheriakova, D. *et al.*, *FASEB J.* **15**:230 (2001); Shen, B.-Q. *et al.*, *J. Biol. Chem.* **276**:5281 (2001).

5   More specifically, sepsis has been characterized by systemic activation of inflammation and blood coagulation. Fibrinolyisis can be suppressed. Some research has pointed to a hemostatic imbalance that is thought to promote e.g., DIC and microvascular thrombosis. These and related indication are believed to impact normal organ function which can lead to death.

10

Sepsis and related disorders continue to be linked to patient contact with hospitals and out-patient clinics. Accordingly, managing these disorders is a prime concern of many health administrators, clinicians and insurers.

15   There are reports that undesired activation of blood coagulation is a key feature of certain inflammatory diseases. For example, extravascular fibrin deposition has been found in the autoimmune lesions of patients with rheumatoid arthritis (RA), glomerulonephritis, multiple sclerosis, psoriasis, Sjogren's syndrome and inflammatory bowel disease. See Weinberg, *et al.*, *Arthritis Rheum.* **34**:996-1005
20   (1991); Wakefield, *et al.*, *J Clin Pathol* **47**:129-133 (1994); Schoph, *et al.*, *Arch Dermatol Res* **285**:305-309 (1993); Zeher, *et al.*, *Clin Immunol Immunopathol* **71**:149-155 (1994); More, *et al.*, *J Clin Pathol* **46**:703-708 (1993).

Moreover, elevated TF levels are thought to be associated with systemic lupus
25   erythematosus. See Segal, *et al.*, *J Rheumatol* **27**:2827-2832 (2000). See also Nakano, *et al.*, *Clin Exp Rheumatol* **17**:161-170 (1999); Morris, *et al.*, *Ann Rheum Dis* **53**:72-79 (1994); Furmaniak-Kazmierczak, *et al.*, *J Clin Invest* **94**:472-480 (1994); Bokarewa, *et al.*, *Inflamm Res* **51**:471-477 (2002).

30   There have been suggestions that certain inflammatory conditions may be treated by blocking thrombosis. See R. Gordon *et al.*, *The New England Journal of*

Medicine **344**:699-709, 759-762 (2001). Certain anti-TF antibodies have been reported to be of some help in reducing some types of inflammation. See Levi, M. *et al., supra.*

5   There have been efforts to develop antibodies that bind blood coagulation factors.

For instance, U.S. Pat. Nos. 5,986,065 and 6,555,319 to Wong, H. *et al.* and PCT/US98/04644 (WO 98/40408) disclose a variety of such antibodies. Specifically

10   provided are murine antibodies, chimeric antibody derivatives and fragments thereof with significant binding affinity and specificity for tissue factor (TF). Use of chimeric antigen binding molecules are believed to reduce risk of an undesired immune response in human patients. See also S. L.Morrison and V. Oi, *Adv. Immunol.* **44**:65 (1989) (reporting methods of making human-mouse chimeric

15   antibodies).

A variety of approaches have been used to make antibodies more immunologically acceptable to humans. Some use recombinant DNA technologies. For instance, one strategy has been to clone and modify non-human antibodies to

20   more closely resemble human antibodies. Collectively, such antibodies have been referred to as "humanized". See U.S Pat. Nos. 5,766,886 to Studnicka *et al.*; 5,693,762 to Queen *et al.*; 5,985,279 to Waldeman *et al.*; 5,225,539 to Winter; 5,639,641 to Pedersen, *et al.*; and references cited therein for methods of making and using humanized antibodies.

25

Additional strategies for making humanized antibodies have been reported. See E. Padlan *Mol. Immunol.* **28**:489 (1991); Jones *et al., Nature* **321**:522-525 (1986); Junghans *et al., supra*; and Roguska, *et al., PNAS (USA)* **91**:969 (1994). See also published U.S Patent Applications 2003/0109860 A1 and 2003/0082636.

30

It is unclear if prior antibodies are robust enough to block or reduce undesired activation of blood coagulation. More specifically, it is unclear if such antibodies are potent enough to prevent or treat sepsis and inflammatory diseases such as arthritis.

5   **SUMMARY OF THE INVENTION**

The present invention features compositions and methods for preventing or treating disorders relating to undesired activation of blood coagulation. In one aspect, the invention provides methods for preventing or treating such disorders by administering to a mammal a therapeutically effective amount of a chimeric or

10   humanized antibody that binds tissue factor (TF). The invention has a wide spectrum of important applications including use in the treatment of sepsis and inflammatory diseases such as arthritis.

We have found that antibodies and antigen binding fragments thereof that

15   specifically bind an epitope predominant to native human TF are suitable for preventing or treating disorders relating to undesired activation of blood coagulation. Preferred antibodies and fragments specifically bind native human TF and do not substantially bind non-native or denatured TF. More particular antibodies and fragments suitable for use with the present invention bind human TF so that at least

20   one of Factor X (FX) and Factor IX (FIX) do not effectively bind to the TF-Factor VIIa complex. Additionally preferred antibodies and fragments reduce or block TF function, typically by reducing or blocking FX binding or gaining access to TF molecules. Further preferred antibodies and fragments suitable for use with the invention do not significantly inhibit or block interaction or binding between TF and

25   Factor VIIa, or inhibit or block activity of a TF-Factor VIIa complex with respect to materials other than FX or FIX.

As discussed, it is believed that undesired activation of blood coagulation underlies sepsis and a variety of specific inflammatory diseases. More specifically,

30   unwanted TF-mediated coagulation is thought to initiate and/or prolong such disorders in many cases. It is thus an object of the present invention to provide

antibodies and fragments thereof that specifically bind TF to reduce or inactivate
many if not all TF-associated functions. Such functions include, but are not limited
to, blocking or inhibiting at least one of FIX and FX binding to the TF complex.
Without wishing to be bound to theory, it is believed that by blocking or inhibiting

5   binding of at least one of those factors to the TF complex, activation of unwanted
blood coagulation can be reduced or in some cases eliminated. That is, by blocking
or inhibiting such unwanted processes according to the invention, it is believed that it
is possible to prevent, treat or alleviate symptoms associated with sepsis and specific
inflammatory diseases.

10

Preferably, such antibodies and fragments thereof are chimeric or humanized
and are generally suitable for use in primates and particularly human patients in need
of treatment.

15 There is recognition that sepsis and related conditions result from a potent and
potentially life-threatening immune response to infection, trauma, or both. Typically,
blood throughout the vasculature is subject to coagulation, resulting in complications
such as inflammation, disseminated intravascular coagulation (DIC), clotting, and
organ distress. Death can ensue in a matter of hours or less unless the condition is

20 treated rapidly. Prior to the present invention, it was not clear if any anti-TF antibody
or TF-binding fragment would be robust enough to prevent or treat sepsis and related
conditions.

However, it has been found that the anti-TF binding antibodies described

25 herein are robust enough (i.e., bind human TF specifically enough and with
appropriate avidity) to inhibit or block unwanted activation of the coagulation
cascade. It has also been found that such activity is beneficial and can be used to
prevent or treat sepsis and related conditions. As discussed below, we have found
that such antibodies and fragments show good attenuation of inflammation,

30 disseminated intravascular coagulation (DIC), clotting, organ distress and related
conditions in an in vivo animal model of human sepsis.

6

Such potent blocking or inhibition of the blood coagulation cascade has also been found to be highly useful in the prevention or treatment of certain inflammatory diseases. Without wishing to be bound to theory, it is believed that by using the

5   invention to block or reduce undesired activation of blood coagulation, it is possible to prevent, treat or alleviate symptoms associated with one or a combination of the inflammatory diseases. Importantly, the anti-TF binding antibodies described herein have been found to be robust enough to inhibit or block unwanted activation of the coagulation cascade, thereby helping to prevent, treat or alleviate symptoms

10   associated with arthritis and other inflammatory diseases.

Accordingly, and in one aspect, the invention provides a method for preventing or treating at least one of sepsis and an inflammatory disease in a mammal. In one embodiment, the method includes administering to the mammal a

15   therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to human TF to form a complex. A more preferred antibody reduces or blocks at least one of FX and FIX binding to the complex. Practice of the method is highly useful for preventing, treating, or reducing the severity of symptoms associated with sepsis and inflammatory diseases

20   including, but not limited to, rheumatoid arthritis (RA).

The present invention provides other important uses and advantages.

For instance, we have discovered that preferred humanized antibodies,

25   chimeric antibodies and fragments thereof desirably block at least one of FX and FIX binding to the TF-FVIIa complex. Preferably, such antibodies and fragments also inhibit or block FX or FIX activation by the complex. Surprisingly, such antibodies, when tested in the *in vivo* animal of human sepsis provided herein, are robust enough to prevent, treat or alleviate symptoms of sepsis and related complications. Also

30   surprisingly, such preferred antibodies and fragments are robust enough to prevent, treat, or alleviate symptoms associated with particular inflammatory diseases.

Importantly, preferred use of the present invention has identified and takes advantage of a particular immunological target (epitope) on the human TF molecule that can be exploited to prevent, treat, or alleviate symptoms associated with these indications.

5   The invention is flexible and can be used in a variety of settings in which sepsis and inflammatory diseases may be suspected or predominate.

For instance, and in one embodiment, the invention can be used in hospitals, clinics and other medical settings where sepsis has become a major health problem. Especially problematic has been emergence of antibiotic resistance microorganisms such as bacteria which, if present in the blood, can rapidly produce septic shock and related complications. Practice of the invention can be used to hold the sepsis or related condition at bay while caregivers identify an appropriate treatment protocol, or perhaps reverse the effects of sepsis. It is thus anticipated as an object of the invention to provide sepsis prevention or treatment methods in which administration of the antibodies and fragments disclosed herein may be combined with administration of one or more antibiotics.

The invention finds further use in emergency medical settings (*e.g.*, ambulance, combat) in which the prevention and treatment methods disclosed herein can be administered at the point of care. Thus in one invention embodiment, the sepsis or sepsis-related condition can be held under some control while the patient is transported to a hospital or clinic for evaluation and treatment.

25   In other invention embodiments, the invention can be used to prevent, treat or reduce symptoms associated with arthritis and especially rheumatoid arthritis. For instance, by blocking or reducing the unwanted activation of blood coagulation, it is now possible to reduce the painful inflammation, pathological tissue destruction and remodeling typically associated with arthritis and related inflammatory diseases.

30

In another aspect, the invention provides a kit for performing the methods of this invention. In one embodiment, the kit includes at least one humanized antibody, chimeric antibody, or fragment thereof provided herein.

5   The invention also provides a method for reducing cytokine production in a mammal. In one embodiment, the method includes administering to the mammal a therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to tissue factor (TF) to form a complex. Preferably, Factor X or Factor IX binding to the complex is inhibited and
10   the administration is sufficient to reduce the cytokine production in the mammal. Suitable humanized antibodies, chimeric antibodies and fragments thereof are disclosed above and in the discussion and examples that follow.

Further provided by the present invention is a method for preventing or
15   treating a sepsis-related condition in a mammal. In one embodiment, the method includes administering to the mammal a therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to tissue factor (TF) to form a complex. Preferred antibodies and fragments are described herein and include those in which Factor X or factor IX
20   binding to the complex is inhibited. Preferably, administration is sufficient to prevent or treat the condition in the mammal.

The invention further provides a method for preventing or treating sepsis-induced anemia in a mammal. In one embodiment, the method includes
25   administering to the mammal a therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to tissue factor (TF) to form a complex. Preferred antibodies and fragments are disclosed herein including those in which Factor X or Factor IX binding to the complex is inhibited. Preferably, the administration is sufficient to prevent or treat
30   the condition in the mammal.

Other aspects of the invention are discussed *infra*.

BRIEF DESCRIPTION OF THE DRAWINGS

Figs. 1A and 1B shows the nucleic acid (SEQ ID NOS: 1 and 3) and amino
5 acid (SEQ ID NOS: 2 and 4) sequences of light chain and heavy chain variable
domains of H36.D2.B7, the murine anti-tissue factor antibody, with hypervariable
regions (CDRs or Complementarity Determining Regions) underlined (single
underline for nucleic acid sequences and double underline for amino acid sequences).

10 Fig. 2 is a drawing showing a plasmid map of humanized anti-TF IgG1
antibody expression vector (pSUN-34).

Figs. 3A-D are sequences of partially and fully humanized light chain (LC)
variable domains of the anti-TF antibody (SEQ ID NO.: ____). Fig. 3A shows the
15 sequence named "LC-09" which is representative of a fully humanized LC
framework (SEQ ID NO.:____). Light chain CDR sequences of cH36 and LC-09 are
shown in Figs. 3B-D (SEQ ID NOS.: _____, respectively).

Figs. 4A-D are drawings showing the sequences of partially and fully
20 humanized heavy chain (HC) variable domains of the anti-TF antibody (SEQ ID
NOS.: _____). Fig. 4A shows the sequence named "HC-08" which is representative
of a fully humanized HC framework (SEQ ID NO.:____). Heavy chain CDR
sequences for cH36 and HC-08 are shown in Figs. 4B-D (SEQ ID NOS.: _____,
respectively).
25

Figs. 5A-B are sequences showing human constant domains in the IgG1 anti-
tissue factor antibody (hOAT), with Fig. 5A showing the human kappa light chain
constant domain (SEQ ID NO.: ____) and Fig. 5B showing the human IgG1 heavy
chain constant domain (SEQ ID NO.: ___). The figures show hOAT (IgG1) constant
30 domain amino acid sequences.

Figs. 6A-B are sequences showing human constant domains in the IgG4 anti-tissue factor antibody (hFAT) with Fig. 6A showing the human kappa light chain constant domain (SEQ ID NO.: ____) and Fig. 6B showing the human IgG4 heavy chain constant domain (SEQ ID NO.: _____).

5

Figs. 7A-D are graphs showing a change in plasma IL-6 and IL-8 (Figs. 7A-B) concentrations (Figs. 7A-B); or IL-1β and TNF-α concentrations (Figs. 7C-D) in rhesus monkeys following an infusion of live *E.coli* in a lethal sepsis model.

10   Figs. 8A-C are graphs showing that cH36 attentuates sepsis-induced acute lung injury (ALI). In the figures, AaDO$_2$ is in mmHg, time in hours, pulmonary system compliance (Cst) in ml/cm water, and pulmonary arterial pressure (PAM) in mmHg.

15   Figures. 9A-B are graphs showing Kidney Myeloperoxidase (A) and Small Bowel Wet/Dry Weight Ratio (B) in Baboons.

Figure 10A-D are graphs showing that cH36 attenuates sepsis and related conditions in baboons. cH36 attenuates sepsis-induced coagulopathy (fibrinogen in 20   mg/DL; time in hours; partial prothrombin time (PTT) in seconds; and TAT in micrograms/L).

Figures 11A-B are graphs showing that elevations in serum IL-8 (A) and IL-6(B) are attenuated by treatment with cH36.

25

Figure 12 is a graph showing that elevations in bronchial alveolar levage IL-8, IL-6 and TNFR1 levels attenuated by treatment with cH36.

Figures 13A-C are graphs showing mean urine output (13A), mean blood pH .30   (13B), and serum bicarbonate levels (13C) in baboons treated with control and cH36 antibodies.

DETAILED DESCRIPTION OF THE INVENTION

As discussed, the invention provides a method for preventing, treating, or alleviating symptoms associated with sepsis or inflammatory diseases such as

5   arthritis. Practice of the method involves administering to a mammal in need of such treatment a therapeutically effective amount of at least one of a humanized antibody, chimeric antibody, or human TF-binding fragment to prevent or treat these diseases and related conditions.

10   There have been efforts to understand the etiology of sepsis and conditions related to sepsis. For instance, there is recognition that early events in the sepsis cascade are triggered by the host's immune response, thereby facilitating damaging actions on the vascular endothelium. Subendothelial structures are exposed and collagenases are liberated. Endothelial cells expressing tissue factor (TF) are

15   exposed, triggering the extrinsic pathway for activation of the coagulation cascade and accelerating the production of thrombin. Concurrently, the endothelial damage causes further exacerbation of inflammation, resulting in neutrophil activation, neutrophil-endothelial cell adhesion, and further elaboration of inflammatory cytokines. These inflammatory processes further contribute to vascular endothelial

20   dysfunction. Endogenous modulators of homeostasis, such as protein C and anti-thrombin III (AT III), are consumed and their levels become deficient as the body attempts to return to a normal functional state. Under normal conditions, the endothelial surface proteins thrombomodulin and endothelial protein C receptor (EPCR), activate protein C and its modulating effects. In sepsis, the endothelial

25   damage impairs this function of thrombomodulin and EPCR, thereby contributing to the loss of control. Left unopposed, the endothelial damage accumulates. This uncontrolled cascade of inflammation and coagulation fuels the progression of sepsis, resulting in hypoxia, widespread ischemia, organ dysfunction, and ultimately death for a large number of patients.

30

By the phrase "sepsis-related condition" is meant those known to precede,
accompany, or follow sepsis including, but not limited to, disseminated intravascular
coagulation (DIC), fibrin deposition, thrombosis, and lung injury, including acute
lung injury (ALI), or acute respiratory distress syndrome (ARDS). A particular type

5   of lung injury amenable to prevention or treatment by use of the invention is sepsis-
induced acute lung injury. See Welty-Wolf, *et al., Am. J. Respir. Crit. Care Med.*
164:1988 (2001), for instance. Also encompassed are certain renal disorders
accompanying sepsis such as acute tubular necrosis (ACN) and related conditions.

10   Acute lung injury (ALI) and acute respiratory distress syndrome (ARDS) are
severe disorders that continue to receive significant attention. In particular, an
important feature of ALI and ARDS, is local activation of extrinsic coagulation and
inhibition of fibrinolysis. As the injury evolves, these perturbations have been
reported to cause deposition of fibrin in the microvascular, interstitial, and alveolar

15   spaces of the lung leading to capillary obliteration and hyaline membrane formation.
Components of the extrinsic coagulation pathway (*e.g.* tissue factor (TF), thrombin,
and fibrin) signal alterations in inflammatory cell traffic and increases in vascular
permeability. Procoagulants and fibrin are also thought to promote other key events
in the injury including complement activation, production of pro-inflammatory

20   cytokines, inhibition of fibrinolysis, and remodeling of the injured lung. Without
wishing to be bound to theory, it is believed that by reducing or blocking these
initiating events (extrinsic coagulation) and downstream effects (pro-inflammatory
events) in the lungs, disordered fibrin turnover can be reduced or blocked and the
evolution of severe structural and functional injury can be reduced or averted during

25   ALI/ARDS. Coagulation blockade can target the TF-Factor VIIa (TF-FVIIa)
complex at several points, but the effects of these different strategies on inflammation
and the development of lung injury are still being confirmed. The Examples show
use of a chimerized monoclonal antibody against human TF (cH36) and its Fab
fragment (cH36-Fab) in blocking initiation of coagulation in gram-negative sepsis

30   and prevent acute lung injury.

The present invention is intended, in one embodiment, to prevent or treat sepsis and sepsis related conditions (such as DIC, ALI and ARDS) by reducing or blocking activity of a key component of the blood coagulation cascade (*i.e.*, TF). Preferred humanized antibodies, chimeric antibodies, and fragments thereof

5   specifically bind human TF typically to block at least one of FX or Factor IX binding to the TF complex. Typically, such preferred antibodies and fragments also inhibit or block FX or FIX activation of that complex. Thus, the compositions and methods of the invention reduce or block unwanted activation of the blood coagulation cascade by decreasing or preventing activity of a key molecular component.

10

Such preferred antibodies are different from prior antibodies such as those provided by U.S. Pat. No. 6,274,142 ("'142") to O'Brien et al. For instance, the '142 patent reports TF neutralizing antibodies that cannot bind to Factor VII/VIIa or effect proteolysis of Factors IX or X. In contrast, preferred antibodies of the invention

15   substantially reduce or block at least one of FX or FIX binding to the TF complex. See also PCT/US01/07501 (WO 01/70984).

As mentioned previously, unwanted coagulation activation is a prominent feature of certain inflammatory diseases, particularly those associated with

20   autoimmunity. See Weinberg, *et al.*, *Arthritis Rheum.* 34:996-1005 (1991); Kincaid-Smith, *Kidney Int* 7:242-253 (1975); Wakefield, *et al.*, *J Clin Pathol* 47:129-133 (1994); Schoph, *et al.*, *Arch Dermatol Res* 285:305-309 (1993); Zeher, *et al.*, *Clin Immunol Immunopathol* 71:149-155 (1994); More, *et al.*, *J Clin Pathol* 46:703-708 (1993). Elevated TF levels have been reported to be associated with disease activity

25   in systemic lupus erythematosus. See Segal, *et al.*, *J Rheumatol* 27:2827-2832 (2000). It is thus an object of this invention to help control tissue factor-mediated coagulation, thereby reducing or in some instances blocking the inflammation, pathological tissue destruction and undesired remodeling that is a hallmark of many inflammatory diseases.

30

14

By the phrase "inflammatory disease" including plural forms is meant a pathological condition associated with an unwanted TF-mediated activation of the coagulation. Preferred inflammatory diseases are usually associated with a known or suspected autoimmune condition. Typically, such diseases are further associated with

5   enhanced production of pro-inflammatory cytokines and/or chemokines as determined by standard methods. Examples of such cytokines include IL-1, TNFα, GM-CSF, M-CSF, IL-6, LIF, IL-15, IFNα, and IL12. Examples of such chemokines include IL-8, MIP-1α, MIP-1β, MCP-1, ENA-78, and RANTES. Typically, but not exclusively, one or more of neovascularization and extravascular fibrin deposition is

10   associated with the inflammatory disease. More particular examples of inflammatory diseases according to the invention include arthritis, preferably rheumatoid arthritis (RA); glomerulonephritis, multiple sclerosis, psoriasis, Sjogren's syndrome and inflammatory bowel disease. Arthritis can be readily detected by one or a combination of features including presence of synovial inflammation, pannus

15   formation, and cartilage destruction.

Preferred use of the invention will help reduce, prevent or alleviate symptoms of the inflammatory disease typically by decreasing TF-mediated coagulation activation. Such activation by TF is believed to provide many disadvantages

20   including, but not limited to, supporting the production of inflammatory molecules, enhancing proinflammatory cell activity, increasing tissue destruction, increasing unwanted remodeling and boosting angiogenesis. The invention thus provides a new and fundamental means for addressing inflammatory disease by providing compositions and methods for specifically binding and inhibiting function of TF.

25

Practice of the invention will particularly help in the prevention and treatment of inflammatory autoimmune diseases. Recent work is in agreement with this inventive concept. See Marty, *et al.*, *J Clin Invest* **107**:631-640 (2001); Varisco, *et al.*, *Ann Rheum Dis* **59**:781-787 (2000); Busso, *et al.*, *Arthritis Rheum* **48**:651-659

30   (2003).

As discussed, the U.S. Pat. Nos. 5,986,065 and 6,555,319 to Wong, H. *et al.* and PCT/US98/04644 (WO 98/40408) disclose a variety of murine anti-TF antibodies and antigen binding fragments with good human TF binding characteristics. Such

5   antibodies and fragments can be employed in accord with the present invention. Additionally, such antibodies and fragments can be used to treat experimentally induced sepsis, for instance, in a relevant rodent model. However, and as will be appreciated, such murine antibodies and fragments are not usually appropriate for use in other mammals such as primates and especially human subjects. Further suitable

10   antibodies and fragments are disclosed by U.S. Patent Application Publication No. 20030082636; WO 03/037911 and WO 98/40408.

By the phrase "antigen binding fragment" is meant at least a part of an antibody that specifically binds antigen. An example of such a fragment includes an

15   antibody V domain. Examples of a suitable V domain binding partner include a C domain and acceptable fragments thereof. Further suitable fragments include parts of the V domain having a combined molecular mass for the V domain of between from about 15 kilodaltons to about 40 kilodaltons, preferably between from about 20 kilodaltons to about 30 kilodaltons, more preferably about 25 kilodaltons as

20   determined by a variety of standard methods including SDS polyacrylamide gel electrophoresis or size exclusion chromatography using appropriately sized marker fragments, mass spectroscopy or amino acid sequence analysis. Further specific antigen binding fragments include Fab, F(v), Fab', F(ab')$_2$ and certain single-chain constructs that include the antibody V domain.

25

Additionally suitable antigen binding fragments include at least part of an antigen binding V domains alone or in combination with a cognate constant (C) domain or fragment thereof ("cognate" is used to denote relationship between two components of the same immunoglobulin heavy (H) or light (L) chain). Typical C

30   domain fragments have a molecular mass of between from about 5 kilodaltons to about 50 kilodaltons, more preferably between from about 10 kilodaltons to about 40

kilodaltons, as determined by a variety of standard methods including SDS
polyacrylamide gel electrophoresis or size exclusion chromatography using
appropriately sized marker fragments, mass spectroscopy or amino acid sequence
analysis. Additionally suitable antigen binding fragments are disclosed below as well

5   as in U.S. Pat. Nos. 5,986,065 and 6,555,319 to Wong, H. *et al.* and
PCT/US98/04644 (WO 98/40408). See also U.S. Patent Application Publication No.
20030082636 and the following International Applications: WO 03/037911 and WO
98/40408.

10

    As also mentioned, one approach to minimize any potential immunorejection
by primate hosts such as human patients is to make a chimeric antibody. By the
phrase "chimeric antibody" or related phrase including plural forms is meant
antibodies as disclosed herein whose light and heavy chain genes have been

15   constructed, typically by genetic engineering, from immunoglobulin gene segments
belonging to different species, usually a primate and preferably a human. For
example, the variable (V) domains of the genes from a mouse antibody such as H36
may be joined to human constant (C) domains, such as γ_1, γ_2, γ_3, or γ_4. A typical
therapeutic chimeric antibody is thus a hybrid protein consisting of the V or antigen-

20   binding domain from a mouse antibody and the C or effector domain from a human
antibody, although other mammalian species may be used. A specifically preferred
chimeric antibody for use with the invention is the anti-tissue factor antibody cH36
disclosed below in the Examples.

25   Suitable chimeric antibodies for use with the invention can be made by one or
a combination of known strategies. As disclosed in the U.S. Pat. Nos. 5,986,065,
6,555,319 and PCT/US98/04644 (WO 98/40408), a highly useful murine anti-TF
antibody can be readily obtained from a variety of sources including the American
Type Culture Collection (ATCC, 10801 University Boulevard, Manassas, VA

30   20110). The antibody has been deposited as ATCC Accession No. HB-12255.
Alternatively, suitable antibodies can be made *de novo* (as polyclonal or monoclonal

as needed) in accord with procedures disclosed in the U.S. Pat. Nos. 5,986,065 and 6,555,319 for instance.

See also U.S. Patent Application Publication No. 20030082636 and the

5   following International Applications: WO 03/037911 and WO 98/40408.

The antibody deposited with the ATCC H36 is referred to herein as H36. It is also referenced as H36.D2 and as H36.D2.B7. The antibody designated as H36 is the antibody produced by the mother clone, and H36.D2 is obtained from the primary

10   clone, whereas H36.D2.B7 is obtained from the secondary clone. No differences were observed between the antibody produced by those three clones with respect to the antibody's ability to inhibit TF or other physical properties. In general usage, H36 is often used to indicate anti-TF antibody produced by any of these clones or related cell lines producing the antibody. The mouse-human chimeric version of H36

15   is referred to cH36 (and also as Sunol-cH36). See also the U.S. Pat. No. 5,986,065 and PCT/US98/04644 (WO 98/40408) for more specific information about the H36 antibody.

A preferred chimeric antibody combines the murine variable domain from a

20   suitable antibody such as H36 and a human constant domain. The manipulation is usually achieved by using standard nucleic acid recombination techniques. A variety of types of such chimeric antibodies can be prepared, including *e.g.* by producing human variable domain chimeras, in which parts of the variable domains, especially conserved regions of the antigen-binding domain, are of human origin and only the

25   hypervariable regions are of non-human origin. See S.L. Morrison, *Science*, **229**:1202-1207 (1985); Oi *et al.*, *BioTechniques* **4**:214 (1986); Teng *et al.*, *Proc. Natl. Acad. Sci. U.S.A.*, **80**:7308-7312 (1983); Kozobor *et al.*, *Immunology Today* **4**:72-79 (1983); Olsson *et al.*, *Meth. Enzymol.* **92**:3-16 (1983); U.S. Pat. No. 5,986,065; and PCT/US98/04644 (WO 98/40408).

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Nucleic acids encoding the H36 variable and constant regions have been disclosed in the U.S. Pat. No. 5,986,065; and PCT/US98/04644 (WO 98/40408), for example. See also U.S. Patent Application Publication No. 20030082636; WO 03/037911 and WO 98/40408.

In one embodiment, the anti-TF chimeric antibody will include a human light chain constant (C) domain *i.e.*, Cκ, C$_\lambda$ or a fragment thereof. Often, the humanized light chain fragment will have an amino acid length of between from about 80 to about 250 amino acids, preferably between from about 95 to about 235 amino acids, more preferably between from about 104 to about 225 amino acids. The size of the humanized light chain fragment can be determined by a variety of standard methods including SDS polyacrylamide gel electrophoresis or size exclusion chromatography using appropriately sized marker fragments, mass spectroscopy or amino acid sequence analysis.

Typically, the chimeric antibody for use in the present methods further includes a human heavy chain variable (V) domain having an amino acid length of between about 80 to about 650 amino acids, preferably between from about 95 to about 540 amino acids, more preferably about 102 to about 527 amino acids as determined *e.g.*, by standard SDS polyacrylamide gel electrophoresis or size exclusion chromatography using appropriately sized marker fragments; mass spectroscopy or amino acid sequence analysis.

Nucleic acid sequence encoding suitable human light chain C and V domains have been reported. See *e.g.*, Kabat *et al.* in *Sequences of Proteins of Immunological Interest* Fifth Edition, U.S. Dept. of Health and Human Services, U.S. Government Printing Office (1991) NIH Publication No. 91-3242; and GenBank. See the National Center for Biotechnology Information (NCBI)- Genetic Sequence Data Bank (Genbank) at the National Library of Medicine, 38A, 8N05, Rockville Pike, Bethesda, MD 20894. See Benson, D.A. *et al.*, *Nucl. Acids. Res.* 25:1 (1997) for a more specific description of Genbank.

Suitable recombinant techniques for use in making the chimeric antibodies and other antibodies and fragments as reported herein have been disclosed. See generally Sambrook *et al.* in *Molecular Cloning: A Laboratory Manual* (2d ed. 1989); and Ausubel *et al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, (1989).

For some invention applications in which a minimal immunoresponse against an anti-TF antibody is needed, it will be useful to prepare humanized antibodies. By the phrase "humanized" is meant an immunoglobulin that includes at least one human FR subset, preferably at least two or three of same, more preferably four human FR subsets, and one or more CDRs from a non-human source, usually rodent such as a rat or mouse immunoglobulin. Typically preferred humanized immunoglobulins of the invention will include two or more preferably three CDRs. Constant domains need not be present but are often useful in assisting function of humanized antibodies intended for *in vivo* use. Preferred constant domains, if present, are substantially identical to human immunoglobulin constant domains *i.e.*, at least about 90% identical with regard to the amino acid sequence, preferably at least about 95% identical or greater. Accordingly, nearly all parts of the humanized immunoglobulin, with the possible exception of the CDRs, are preferably substantially identical to corresponding parts of naturally occurring human immunoglobulin sequences.

Methods for determining amino acid sequence identity are standard in the field and include visual inspection as well as computer-assisted approaches using BLAST and FASTA (available from the National Library of Medicine (USA) website). Preferred matching programs for most embodiments are available from website for the international ImMunoGeneTics (IMGT) database and a more preferred matching program for this embodiment is the program called Match which is available in the Kabat database. See Johnson G, Wu T. "Kabat database and its application: Future directions." *Nucleic Acids Res*. 29:205-206 (2001).

By the phrase "humanized antibody" is meant an antibody that includes a humanized light chain and a humanized heavy chain immunoglobulin. See S.L. Morrison, *supra*; Oi *et al.*, *supra*; Teng *et al.*, *supra*; Kozbor *et al.*, *supra*; Olsson *et al.*, *supra*; and other references cited previously. Accordingly, a "humanized antibody fragment" means a part of that antibody, preferably a part that binds antigen specifically.

The H36 or cH36 antibody can be humanized by one or a combination of approaches as described, for example, in U.S Pat. Nos. 5,766,886; 5,693,762; 5,985,279; 5,225,539; EP-A-0239400; 5,985,279 and 5,639,641, or as disclosed in the published U.S. application number 20030190705. See also E. Padlan *Mol. Immunol.* **28**:489 (1991); Jones *et al.*, *Nature* **321**:522-525 (1986); Junghans *et al.*, *supra*; and Roguska, *et al. PNAS (USA)* **91**:969 (1994) for additional information on humanizing antibodies.

Particular humanized antibodies and fragments thereof for use with the present invention are disclosed below in the Examples section.

Preferred chimeric antibodies, humanized antibodies, as well as fragments thereof that specifically bind human TF. By the term, "specific binding" or a similar term is meant a molecule disclosed herein which binds another molecule, thereby forming a specific binding pair. However, the molecule does not recognize or bind to other molecules as determined by, *e.g.*, Western blotting ELISA, RIA, mobility shift assay, enzyme-immunoassay, competitive assays, saturation assays or other protein binding assays know in the art. See generally, Sambrook *et al.* in *Molecular Cloning: A Laboratory Manual* (2nd ed. 1989); and Ausubel *et al.*, supra; and Harlow and Lane in *Antibodies: A Laboratory Manual* (1988) Cold Spring Harbor, New York for examples of methods for detecting specific binding between molecules.

Especially suitable chimeric antibodies, humanized antibodies and fragments for use with the invention will feature at least one of: 1) a dissociation constant (K_d)

for the TF of less than about 0.5 nM; and 2) an affinity constant (K_a) for the TF of less than about 10×10^{10} M^{-1}. Methods of preforming such assays are known in the field and include Enzyme-Linked Immuno-Sorbent Assay (ELISA), Enzyme ImmunoAssay (EIA) radioimmunoassay (RIA) and BIAcore analysis.

5

Additionally suitable antibodies will increase survival time in what is sometimes referred to herein as a "standard *in vivo* septic shock assay". Generally, such an assay involves administering gram-negative bacteria to monkeys to induce sepsis. See Taylor *et al. J. Clin. Invest.* **79**:918 (1987). More specifically, a dose of

10   *E. coli* (about 10^{10} CFU/kg) is freshly prepared and administered intravenously to a primate, *e.g.* baboon or rhesus monkey, in a 1-2 hour interval. A control group can receive a saline or PBS injection. The treatment group receives a bolus injection of at least 1 mg/kg antibody, preferably about 10 mg/kg prior to infusion of bacteria *e.g.*, less than about 1 hour before. Control and treatment group monkeys are then

15   monitored for about a week and checked for survival. See the Examples below for more specific information about the standard *in vivo* septic shock assay.

A preferred method of the invention employs a humanized antibody, chimeric antibody or fragment that increases monkey survival time (hours or days) by at least

20   about 2-fold, preferably at least about 3 fold, more preferably at least about 5 fold to 10 fold or more as determined by the standard *in vivo* septic shock assay.

Additionally suitable antibodies for use with the invention can attenuate (reduce presence of at least one of interleukin-6 (IL-6) and interleukin-8 (IL-8) in the

25   plasma of subject mammals after at least about 5 hours following administration of the antibody. Methods for detecting IL-6 and IL-8 and quantifying same from plasma are known and include immunological approaches such as RIA, EIA, ELISA and the like.

30   In one approach, sepsis is induced in a suitable primate such as a monkey and preferably a baboon along lines previously mentioned. Prior to inoculation of control

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baboon (with about 10^{10} CFU/kg *E. coli* or saline), the treatment baboons receive a bolus injection of at least 1 mg/kg antibody, preferably about 10 mg/kg prior to infusion of bacteria *e.g.*, less than about 1 hour before injection of the inoculum. Baboon survival and IL-6 and IL-8 levels in plasma are monitored by standard

5   procedures.

In another approach, a sepsis-like condition is induced in a suitable primate, such as baboon, using a model described as a "primed sepsis model" (see Welty-Wolf, K. *et al. Am. J. Respir. Crit. Care Med.* 164:1988 (2001) and described in

10   further detail in Example 4).

Additionally preferred humanized antibodies, chimeric antibodies and fragments thereof exhibit a blood clotting time of between from about 50 to about 350 seconds as determined by a standard prothrombin (PT) time assay, particularly

15   after about 5 minutes administration of the antibody or fragment to the mammal. An especially useful PT assay has been disclosed in the U.S. Pat. Nos. 5,986,065, 6,555,319 and PCT/US98/04644 (WO 98/40408), for example.

Further preferred antibodies for use in accord with the present invention

20   inhibit platelet deposition by at least about 50% as determined by a standard platelet deposition assay. Methods for performing the assay have been disclosed, *e.g.*, in the pending U.S. Pat. application 10/310,113.

Still further preferred antibodies inhibit collagen-induced arthritis in an

25   experimental mouse model. See Example 5.

"Antibody", "antibody for use with the invention" and like phrases refer to whole immunoglobulin as well as immunologically active fragments which bind a desired antigen. The immunoglobulins and immunologically active (antigen-binding)

30   fragments thereof include an epitope-binding site (*i.e.*, a site or epitope capable of being specifically bound by an antibody recognizing antigen). Exemplary antibody

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fragments include, for example, Fab, F(v), Fab', F(ab')$_2$ fragments, "half molecules" derived by reducing the disulfide bonds of immunoglobulins, single chain immunoglobulins, or other suitable antigen binding fragments (see *e.g.*, Bird *et al.*, *Science*, **242**:423-426 (1988); Huston *et al.*, *PNAS, (USA)*, **85**:5879 (1988); Webber

5   *et al.*, *Mol. Immunol.*, **32**:249 (1995)).

Particular chimeric or humanized antibodies of the present invention can be polyclonal or monoclonal, as needed, and may have, without limitation, an IgG1, IgG2, IgG3 or IgG4 isotype or IgA, IgD, IgE, IgM. An especially preferred antibody

10   for use with the invention has or can be manipulated to have an IgG1 (called "hOAT") or IgG4 (called "hFAT") isotype. Such antibodies can be polyclonal or monoclonal as needed to achieve the objectives of a particular invention embodiment. In some instances, single-chain antibodies such as a humanized single-chain will be preferred.

15

Practice of the invention is applicable to a wide spectrum of mammals. Preferably, the mammal is a primate such as a monkey, chimpanzee, or a baboon. More preferably, the primate is a human patient in need of methods disclosed herein *i.e.*, one that has or is suspected of having sepsis or a sepsis-related condition or an

20   inflammatory disorder or disease.

As discussed above, antibodies of the invention and suitable fragments thereof can be administered to a mammal, preferably a primate such as a human, to prevent or reduce sepsis and related complications. According to one embodiment, such

25   antibodies are used with one or more pharmaceutically acceptable non-toxic carriers such as sterile water or saline, glycols such as polyethylene glycol, oils of vegetable origin, and the like. In particular, biocompatible, biodegradable lactide polymer, lactide glycolide copolymer or polyoxyethylene, polyoxypropylene copolymers may be useful excipients. Other potentially useful administration systems include

30   ethylene vinyl acetate copolymer particles, osmotic pumps, and implantable infusion systems and liposomes. If needed, one or more suitable antibodies or fragments will

be in the form of a solution or suspension (or a lyophilized form that can be reconstituted to a solution or suspension), and will preferably include approximately 0.01% to 10% (w/w) of the antibody of the present invention, preferably approximately 0.01% to 5% (w/w) of the antibody.

5

As discussed, the antibody or fragment can be administered according to the invention as the sole active agent or in combination with other known anti-sepsis therapies. For instance, such antibodies or fragments can be administered to a human patient before, during, or after intervention with one or more appropriate antibotics,

10   typically a broad spectrum intravenous antibiotic therapy. Preferred antibiotics include those known to have broad spectrum anti-microbial activity, covering gram-positive, gram-negative, and anaerobic bacteria. Thus in one embodiment, such antibiotics are given during or after administration of the antibodies and fragments disclosed herein, preferably parenterally in doses adequate to achieve bactericidal

15   serum levels. After stabilizing the patient, various recognized supportive therapies can be used to assist recovery such as administration of oxygen, intravenous fluids, and medications that increase blood pressure. Dialysis may be necessary in the event of kidney failure, and mechanical ventilation is often required if respiratory failure occurs.

20

Persons "at risk" for developing sepsis and related conditions include, but are not limited to, the very old and very young individuals. Also at risk are those with challenged immune systems such as patients infected with a DNA or RNA virus such as HIV or herpes. Nearly any bacterial organism can cause sepsis. Certain fungi and

25   (rarely) viruses may faciliate sepsis and related conditions. Generally, toxins released by the bacteria or fungus may cause direct organ (*e.g.*, lung, kidney) or tissue damage, and may lead to low blood pressure and/or poor organ function. These toxins also produce a vigorous inflammatory response from the body which contributes to septic shock.

30

Additional risk factors include underlying illnesses, such as diabetes; hematologic cancers (lymphoma or leukemia); and other malignancies and diseases of the genitourinary system, liver or biliary system, and intestinal system. Other risk factors are recent infection, prolonged antibiotic therapy, and having been exposed to

5   a recent invasive surgical or medical procedure. Symptoms of sepsis and related conditions are known in the field and include, but are not limited to, fever, chills, lightheadedness, shortness of breath, palpitations, cool and/or pale extremities, fever, agitation, lethargy, and confusion.

10   Success of the invention in the prevention or treatment of sepsis and related conditions can be evaluated by the caregiver using one or a combination of approaches. Typically, a reduction or elimination of one or more of the foregoing symptoms can be taken as indicative that the sepsis or related condition has been addressed. Preferably, patients receiving such treatment will survive at least about 2

15   fold longer than patients who do not receive such intervention.

As discussed, the invention provides a method for reducing cytokine production in a mammal e.g., by administering to the mammal a therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment

20   thereof that binds specifically to tissue factor (TF) to form a complex. Preferably, Factor X or Factor IX binding to the complex is inhibited and the administration is sufficient to reduce the cytokine production in the mammal. Suitable humanized antibodies, chimeric antibodies and fragments thereof are disclosed herein. Acceptable methods for monitoring cytokine production in a mammal are known and

25   include specific methods outlined in the Examples section.

Therapeutic antibodies and fragments in accord with the invention can be used in parenteral or intravenous administration, particularly in the form of liquid

30   solutions. Such compositions may be conveniently administered in unit dose and may be prepared in accordance with methods known in the pharmaceutical art. See

Remington's Pharmaceutical Sciences, (Mack Publishing Co., Easton PA, (1980)).
By the term "unit dose" is meant a therapeutic composition of the present invention
employed in a physically discrete unit suitable as unitary dosages for a primate such
as a human, each unit containing a pre-determined quantity of active material

5   calculated to produce the desired therapeutic effect in association with the required
diluent or carrier. The unit dose will depend on a variety of factors including the type
and severity of sepsis to be treated, general health of the individual, medical history,
and the like. Precise amounts of the antibody to be administered typically will be
guided by judgment of the practitioner, however, the unit dose will generally depend

10   on the route of administration and be in the range of 10 ng/kg body weight to 50
mg/kg body weight per day, more typically in the range of 100 ng/kg body weight to
about 10 mg/kg body weight per day. Suitable regimens for initial administration in
booster shots are also variable but are typified by an initial administration followed
by repeated doses at one or more hour intervals by a subsequent injection or other

15   administration. Alternatively, continuous or intermittent intravenous infusions may
be made sufficient to maintain concentrations of at least from about 10 nanomolar to
10 micromolar of the antibody (or suitable fragment) in the blood.

        Antibodies and fragments for use with the invention are preferably
20   substantially pure when used in the disclosed methods and assays. References to an
antibody being "substantially pure" mean an antibody or protein that has been
separated from components which naturally accompany it. For example, by using
standard immunoaffinity or protein A affinity purification techniques, an antibody of
the invention can be purified from hybridoma or cell culture medium by using native

25   TF as an antigen or protein A resin. Similarly, native TF can be obtained in
substantially pure form by using an antibody of the invention with standard
immunoaffinity purification techniques. Particularly, an antibody or protein is
substantially pure when at least 50% of the total protein (weight % of total protein in
a given sample) is an antibody or protein of the invention. Preferably the antibody or

30   protein is at least 60 weight % of the total protein, more preferably at least 75 weight
%, even more preferably at least 90 weight %, and most preferably at least 98 weight

27

% of the total material. Purity can be readily assayed by known methods such as
SDS polyacrylamide gel electrophoresis (PAGE), column chromatography (*e.g.*,
affinity chromatography, size exclusion chromatography), mass spectroscopy or
HPLC analysis. Preferably, the antibodies and fragments will be used in a sterile

5   format.

        The molecular weight of the antibodies of the invention will vary depending
on several factors such as the intended use and whether the antibody includes a
conjugated or recombinantly fused toxin, pharmaceutical, radioisotope or detectable

10   label or the like. Also the molecular weight will vary depending on nature and extent
of post-translational modifications if any (such as glycosylation) to the antibody. The
modifications are a function of the host used for expression with *E. coli* producing
non-glycosylated antibodies and eucaryotic hosts, such as mammalian cells or plants,
producing glycosylated antibodies. In general, an antibody of the invention will have

15   a molecular weight of between approximately 20 to 150kDa. Such molecular weights
can be readily determined by molecular sizing methods such as SDS-PAGE followed
by protein staining or Western blot analysis.

        It will be apparent that the foregoing method for making the humanized cH36

20   antibody can be readily adapted to make other humanized antibodies and antigen
binding fragments according to the invention.

A. Preparation Of Humanized Anti-Tissue Factor Binding Antibody

25   Preparation and use of a humanized anti-tissue factor binding antibody is
described. See also Examples 1-3 below.

        Briefly, preferred antibodies bind human tissue factor to form a binding
complex. The tissue factor may be naturally occurring or recombinant human (rhTF).

30   Preferably, factor X or factor IX binding to the complex is inhibited. In a preferred
invention embodiment, the humanized antibody has an apparent affinity constant (K_A,

M^{-1}) for the hTF of less than about 1 nM, preferably less than about 0.5 nM, more preferably between from about 0.01 nM to about 0.4 nM. See Examples 1-3, below for more information about determining affinity constants for the humanized antibodies. By "specific binding" is meant that the humanized antibodies form a

5   detectable binding complex with the TF (or rhTF) and no other antigen as determined by standard immunological techniques such as RIA, Western blot or ELISA.

More preferred humanized anti-TF binding antibodies made in accord with this invention exhibit an apparent affinity constant (K_A, M^{-1}) for native human TF of

10   at least about 1 x 10^8 M^{-1} as determined by surface plasmon analysis (particularly, BIACore analysis in accordance with the procedures of Example 3 which follows), more preferably at least about 5 x 10^8 M^{-1} as determined by surface plasmon analysis, still more preferably an apparent affinity constant (K_A, M^{-1}) for native human TF of at least about 3 x 10^9 M^{-1} as determined by surface plasmon resonance analysis. Such

15   substantial binding affinity of antibodies of the invention contrast sharply from much lower binding affinities of previously reported antibodies.

The nucleic acid (SEQ ID NOS. 1 and 3) and amino acid (SEQ ID NOS. 2 and 4) sequences of a particular tissue factor binding antibody that has been

20   humanized by the present methods i.e. H36.D2.B7. See Figures 1A and 1B of the drawings and the PCT application WO 98/40408, for instance. SEQ ID NOS. 1 and 2 are the nucleic acid and amino acid respectively of the light chain variable domain, and SEQ ID NOS. 3 and 4 are the nucleic acid and amino acid respectively of the heavy chain variable domain, with hypervariable regions (CDRs or Complementarity

25   Determining Regions) underlined in all of those sequences.

Additional tissue factor binding humanized antibodies of the invention will have substantial amino acid sequence identity to either one or both of the light chain or heavy sequences shown in Figures 1A and 1B. More particularly, such antibodies

30   include those that have at least about 70 percent homology (amino acid sequence identity) to SEQ ID NOS. 2 and/or 4, more preferably about 80 percent or more

homology to SEQ ID NOS. 2 and/or 4, still more preferably about 85, 90 or 95 percent or more homology to SEQ ID NOS. 2 and/or 4.

5   More particular tissue factor binding humanized antibodies of the invention will have high amino acid sequence identity to hypervariable regions (shown with double underlining in Figures 1A and 1B) of SEQ ID NOS. 2 and 4). Specific antibodies will have one, two or three hypervariable regions of a light chain variable domain that has high sequence identity (at least 90% or 95% amino acid sequence identity) to or be the same as one, two or three of the corresponding hypervariable

10   regions of the light chain variable domain of H36.D2.B7 (those hypervariable regions shown with underlining in Figure 1A and are the following:

     1)   LASQTID (SEQ ID NO. 5);

     2)   AATNLAD (SEQ ID NO. 6); and

     3)   QQVYSSPFT (SEQ ID NO. 7).

15

Additionally specific antibodies that have been humanized by the methods described herein and bind tissue factor will have one, two or three hypervariable regions of a heavy chain variable domain that have high sequence identity (at least 90% or 95% amino acid sequence identity) to or be the same as one, two or three of

20   the corresponding hypervariable regions of the heavy chain variable domain of H36.D2.B7 (those hypervariable regions shown with underlining in Figure 1B and are the following:

     1)   TDYNVY (SEQ ID NO. 8);

     2)   YIDPYNGITIYDQNFKG (SEQ ID NO. 9); and

25   3)   DVTTALDF (SEQ ID NO. 10).

Certain nucleic acids encoding some or all of the antibodies or fragments disclosed herein will preferably have a length sufficient (preferably at least about 100, 200 or 250 base pairs) to bind to the sequence of SEQ ID NO. 1 and/or SEQ ID

30   NO. 3 under the following moderately stringent conditions (referred to herein as "normal stringency" conditions): use of a hybridization buffer comprising 20%

formamide in 0.9M saline/0.12M sodium citrate (6xSSC) buffer at a temperature of 37°C and remaining bound when subject to washing once with that 2xSSC buffer at 37°C.

5   More specifically, certain of the nucleic acids (preferably at least about 100, 200 or 250 base pairs) will bind to the sequence of SEQ ID NO. 1 and/or SEQ ID NO. 3 under the following highly stringent conditions (referred to herein as "high stringency" conditions): use of a hybridization buffer comprising 20% formamide in 0.9M saline/0.12M sodium citrate (6xSSC) buffer at a temperature of 42°C and

10   remaining bound when subject to washing twice with that 1xSSC buffer at 42°C.

Suitable nucleic acids preferably comprise at least 20 base pairs, more preferably at least about 50 base pairs, and still more preferably a nucleic acid of the invention comprises at least about 100, 200, 250 or 300 base pairs.

15

Generally preferred nucleic acids of the invention will express an antibody of the invention that exhibits the preferred binding affinities and other properties as disclosed herein. See also the U.S. Pat. No. 5,986,065 and PCT/US98/04644 (WO 98/40408) for more information.

20

Other appropriate nucleic acids will have substantial sequence identity to either one or both of the light chain or heavy sequences shown in Figures 1A and 1B. More particularly, preferred nucleic acids will comprise a sequence that has at least about 70 percent homology (nucleotide sequence identity) to SEQ ID NOS. 1 and/or

25   3, more preferably about 80 percent or more homology to SEQ ID NOS. 1 and/or 3, still more preferably about 85, 90 or 95 percent or more homology to SEQ ID NOS. 1 and/or 3.

Additionally specific nucleic acid sequences will have high sequence identity

30   to hypervariable regions (shown with underlining in Figures 1A and 1B) of SEQ ID NOS. 1 and 3). Such nucleic acids include those that code for an antibody light chain

variable domain and have one, two or three sequences that code for hypervariable

regions and have high sequence identity (at least 90% or 95% nucleotide sequence

identity) to or be the same as one, two or three of the sequences coding for

corresponding hypervariable regions of H36.D2.B7 (those hypervariable regions

5   shown with underlining in Figure 1A and are the following:

    1) CTGGCAAGTCAGACCATTGAT (SEQ ID NO: 11);

    2) GCTGCCACCAACTTGGCAGAT (SEQ ID NO: 12); and

    3) CAACAAGTTTACAGTTCTCCATTCACGT (SEQ ID NO: 13).

10   More specific nucleic acids also code for an antibody heavy chain variable

domain and have one, two or three sequences that code for hypervariable regions and

have high sequence identity (at least 90% or 95% sequence identity) to or be the same

as one, two or three of the sequences coding for corresponding hypervariable regions

of H36.D2.B7 (those hypervariable regions shown with underlining in Figure 1B and

15   are the following:

    1) ACTGACTACAACGTGTAC (SEQ ID NO. 14);

    2)

        TATATTGATCCTTACAATGGTATTACTATCTACGACCAGAACTTCA

        AGGGC (SEQ ID NO. 15); and

20   3) GATGTGACTACGGCCCTTGACTTC (SEQ ID NO. 16).

    More specific humanized antibodies for use with the methods of this

invention that bind TF are those in which each of framework regions (FRs) 1, 2, 3

and 4 has at least about 90% amino acid sequence identity, preferably at least about

25   95% or greater identity to the light chain FR sequences shown in Figure 3A (SEQ ID

NO. ___), preferably, the sequence shown as "LC-09" in Figure 3A. Additionally

specific humanized antibodies include a light chain constant domain having at least

about 90% amino acid sequence identity, preferably at least about 95% sequence

identity or greater to the sequence shown in Figure 5A (SEQ ID NO. ___) or Figure

30   6A (SEQ ID NO. ___).

Further specific humanized antibodies are those in which each of framework regions (FRs) 1, 2, 3 and 4 has at least about 90% amino acid sequence identity, preferably about 95% identity or greater to the heavy chain sequences shown in Figure 4A (SEQ ID NO. ___), preferably, the sequence shown as "HC-08" in Figure

5   4A. Additional humanized antibodies have a heavy chain constant domain with at least about 90% amino acid sequence identity, preferably at least about 95% identity or greater, to sequence shown in Figure 5B (SEQ ID NO. ___) or Figure 6B (SEQ ID NO. ___).

10   In certain embodiments, the humanized antibody will have an IgG1 (hOAT) or IgG4 (hFAT) isotype as disclosed in the published U.S. application number 20030190705.

       Also provided by the present invention are functional fragments of the
15   humanized antibodies disclosed herein. Examples of such fragments include, but are not limited to, those that bind TF with an affinity constant (Kd) of less than about 1 nM, preferably less than about 0.5 nM, more preferably between from about 0.01 nM to about 0.4 nM. Specifically preferred are antigen binding Fab, Fab', and F(ab)$_2$ fragments.

20

       As discussed, the invention features humanized antibodies that include at least one murine complementarity determining region (CDR), e.g., CDR1, CDR2, CDR3. In one invention embodiment, the antibodies bind specifically to human tissue factor (TF) to form a complex. Typically, the factor X or factor IX binding to TF or TF-

25   FVIIa and activation by TF-FVIIa thereto is inhibited. As mentioned above, preferred CDRs (light and heavy chain) are from a rodent source, typically the mouse.

       In one embodiment of the humanized antibodies of the invention, the
30   antibodies further include at least one human framework region (FR) subset. Preferably, all the FRs (light and heavy chains) are human.

In a more particular embodiment, the first CDR (CDR1) of the heavy chain
hypervariable region that binds human TF is at least 90% identical to the CDR1
amino acid sequence shown in Figure 4B (SEQ ID NO. ___), preferably at least about

5   95% identical or greater to that sequence. Typically, the second CDR (CDR2) of the
heavy chain hypervariable region is at least 90% identical to the CDR2 amino acid
sequence shown in Figure 4C (SEQ ID NO. ___), preferably at least about 95%
identical or greater. Preferably also, the third CDR (CDR3) of the heavy chain
hypervariable region is at least 90% identical to the CDR3 sequence shown in Figure

10   4D (SEQ ID NO. ___), more preferably about 95% identical or greater to that
sequence.

In another invention embodiment, the first CDR (CDR1) of the light chain
hypervariable region that binds human TF is at least 90% identical to the CDR1

15   amino acid sequence shown in Figure 3B (SEQ ID NO. ___), preferably at least about
95% identical or greater. Typically, the second CDR (CDR2) of the light chain
hypervariable region is at least 90% identical to the CDR2 amino acid sequence
shown in Figure 3C (SEQ ID NO. ___), preferably about 95% identical or greater.
Preferably, the third CDR (CDR3) of the light chain hypervariable region is at least

20   90% identical to the CDR3 amino acid sequence shown in Figure 3D (SEQ ID NO.
___), more preferably about 95% identical or greater to that sequence. ·

Additional humanized antibodies suitable for use with the present methods
include a first framework region (FR1) of the heavy chain hypervariable region that

25   binds human TF which FR1 is at least 90% identical to the amino acid sequence
shown in Figure 4A (SEQ ID NO. ___) as "FR1 HC-08", preferably about 95%
identical or greater to that sequence. In one embodiment, the FR1 comprises at least
one of the following amino acid changes: E1 to Q; Q5 to V; P9 to G; L11 to V; V12
to K; Q19 to R; and T24 to A. Preferably, the FR1 includes two, three, four, five, or

30   six of those changes with all of those amino acid changes being preferred for many
applications.

Further humanized antibodies suitably bind human TF and include a second framework region (FR2) of the heavy chain hypervariable region which FR2 is at least 90% identical to the sequence shown in Figure 4A (SEQ ID NO. ▨) as "FR2

5   HC-08", preferably about 95% identical or greater to that sequence. In one embodiment, the FR2 at least one of the following amino acid changes: H41 to P and S44 to G. A preferred FR2 includes both of those amino acid changes.

The invention also features use of humanized antibodies that bind human TF

10 in which a third framework region (FR3) of the heavy chain hypervariable region is at least 90% identical to the sequence shown in Figure 4A (SEQ ID NO. ▨) as "FR3 HC-08", preferably about 95% identical or greater to that sequence. In one embodiment, the FR3 includes at least one of the following amino acid changes: S76 to T; T77 to S; F80 to Y; H82 to E; N84 to S; T87 to R; D89 to E and S91 to T. A

15 preferred FR3 includes two, three, four, five or six of those amino acid changes with all seven of those amino acid changes being generally preferred.

Also featured is use of humanized antibodies that suitably bind human TF and in which the fourth framework region (FR4) of the heavy chain hypervariable region

20 is at least 90% identical to the amino acid sequence shown in Figure 4A (SEQ ID No. ▨) as "FR4 HC-08", preferably at least about 95% identical or greater to that sequence. Preferably, the FR4 includes the following amino acid change: L113 to V.

Additional humanized antibodies bind human TF and also feature a first

25 framework region (FR1) of the light chain hypervariable region which is at least about 90% identical to the amino acid sequence shown in Figure 3A (SEQ ID NO. ▨) as "FR1 LC-09", preferably at least about 95% identical or greater to that sequence. In one embodiment, the FR1 comprises at least one of the following amino acid changes: Q11 to L; L15 to V; E17 to D; and S18 to R. A preferred FR1

30 includes two or three of such amino acid changes with all four amino acid changes being generally preferred.

35

The present invention also features use of humanized antibodies that bind human TF and in which a second framework region (FR2) of the light chain hypervariable region is at least about 90% identical to the amino acid sequence

5   shown in Figure 3A (SEQ ID NO. ___) as "FR2 LC-09", preferably at least about 95% identical or greater to that sequence. A preferred FR2 has the following amino acid change: Q37 to L.

Also encompassed by the invention is use of particular humanized antibodies

10   that bind human TF in which a third framework region (FR3) of the light chain hypervariable region is at least about 90% identical to the amino acid sequence shown in Figure 3A (SEQ ID NO. ___) as "FR3 LC-09", preferably at least about 95% identical or greater to that sequence. In one embodiment, the FR3 has at least one of the following amino acid changes: K70 to D, K74 to T, A80 to P, V84 to A,

15   and N85 to T. Preferably, the FR3 has two, three, or four of such amino acid changes with all five of the changes being generally preferred.

Additional humanized antibodies appropriate for use with the methods disclosed herein bind TF and include a fourth framework region (FR4) of the light

20   chain hypervariable region which FR4 is at least about 90% identical to the sequence shown in Figure 3A (SEQ ID NO. ___) as "FR4 LC-09", preferably at least about 95% identical or greater to that sequence. In one embodiment, the FR4 includes at least one and preferably all of the following amino acid changes: A100 to Q and L106 to I.

25

The invention also features a human TF binding fragment of the foregoing humanized antibodies. Examples of such fragments include Fab, Fab', and F(ab)$_2$. See the published U.S. application number 20030190705 and references cited therein for additionally preferred humanized anti-TF antibodies made in accord with this

30   invention.

The following three nucleic acid vectors pSUN36 (humanized anti-TF
antibody Ig G1-HC expression vector), pSUN37 (humanized anti-TF antibody Ig G4-
HC expression vector), and pSUN38 (humanized anti-TF antibody LC expression
vector) have been deposited pursuant to the Budapest Treaty with the American Type

5   Culture Collection (ATCC) at 10801 University Boulevard, Manassas VA 20110-
2209. The vectors were assigned the following Accession Numbers: PTA-3727
(pSUN36); PTA-3728 (pSUN37); and PTA-3729 (pSUN38).

Suitable expression and purification strategies for making and using the
10   humanized anti-TF antibodies of this invention have been disclosed in the published
U.S. application number 20030190705, for instance.

As discussed, the invention also provides useful kits for performing one or
more of the methods provided herein. In one embodiment, the kit includes at least
15   one humanized antibody, chimeric antibody, or fragment thereof that binds
specifically to human tissue factor (TF) to form a complex, wherein factor X or factor
IX binding to the complex is inhibited. Typically also, the humanized antibody,
chimeric antibody, or fragment thereof is provided in a pharmaceutically acceptable
vehicle such as saline, water or buffer. The kit may include a pharmaceutically
20   acceptable vehicle for dissolving the humanized antibody, chimeric antibody or
fragment prior to use.

The following non-limiting examples are illustrative of the invention. In the
following examples and elsewhere the method of the invention is applied to the
25   humanization of the murine anti-tissue factor antibody H36. See the U.S Patent Nos.
5,986,065 and 6,555,319; U.S. Patent Application Publication No. 20030082636;
WO 03/037911 and WO 98/40408, and the published U.S. patent application number
20030190705 and references cited therein as well as the discussion above.
Sometimes, the Fab fragment of H36 or cH36 will be referred to as "H36-Fab" and
30   "cH36-Fab", respectively, for the sake of convenience.

All documents mentioned herein are fully incorporated by reference in their entirety.

EXAMPLE 1 – Humanization of Anti-Tissue Factor Antibody

5   The description of how to make and use a particular murine antibody called H36.D2 (sometimes also called H36 as discussed above) is described in U.S. Pat. Nos. 5,986,065 and 6,555,319. The present example shows how to make and use a humanized version of that antibody. A humanized H36 antibody has a variety of uses including helping to minimize potential for human anti-mouse antibody (HAMA)

10   immunological responses. These and other undesired responses pose problems for use of the H36 antibody in human therapeutic applications.

         A. Preparation of chimeric anti-tissue factor antibody (cH36)

15   The H36 antibody described previously is an IgG2a murine antibody. H36 was first converted to a mouse-human chimeric antibody for clinical development. To do this, the heavy and light chain genes for H36 were cloned (see U.S. Patent No. 5,986,065). The heavy chain variable domain was fused to a human IgG4 constant (Fc) domain and the light chain variable domain was fused to a human kappa light

20   chain constant domain. The resulting IgG4κ chimeric antibody was designated cH36 (and is also referred to as Sunol-cH36). For multiple uses of H36 or cH36 in patients with chronic diseases, a fully humanized cH36 is preferred so that it will decease or eliminate any human anti-chimeric antibody (HACA) immunological response. The humanization of cH36 is described below.

25

         B. Humanization Strategy for cH36 Antibody

         Humanization of the chimeric anti-tissue factor antibody cH36 was achieved by using a "FR best-fit" method of the invention. This method takes full advantage

30   of the fact that a great number of human IgGs with known amino acid sequences or sequences of human IgG fragments are available in the public database. The

sequences of the individual framework regions of the mouse heavy and light variable domains in cH36 are compared with the sequences respective heavy or light chain variable domains or human frameworks (or fragments thereof) in the Kabat database (see *e.g.*, Kabat *et al.* in *Sequences of Proteins of Immunological Interest* Fifth

5   Edition, U.S. Dept. of Health and Human Services, U.S. Government Printing Office (1991) NIH Publication No. 91-3242 or http://immuno.bme.nwu.edu). The following criteria were used to select the desired human IgG framework region subsets for humanization: (1) The number of mismatched amino acids was kept as low as possible. (2) Amino acids inside the "vernier" zone (amino acids in this zone may

10   adjust CDR structure and fine-tune the fit to antigen, see Foote, J. and Winter, G., *J. of Mol. Bio.* **224(2)**:487-499 [1992]) were left unchanged. (3) Conservative amino acid substitutions were favored when evaluating similar candidates. The matching program used for this comparison can be found in Kabat database. See Johnson G, Wu T. "Kabat database and its application: Future directions." *Nucleic Acids Res.*

15   **29**:205-206 (2001). The program finds and aligns regions of homologies between the mouse sequences and human sequences in the Kabat's database. By using this unique FR best-fit method, it is anticipated that the humanized LC or HC variable domains of the target IgG may have all the four FRs derived from as few as one human IgG molecule or to as many as four different human IgG molecules.

20

B(i). Selection of Human IgG Kappa Light Chain Variable Domain Framework Regions

The amino acid sequence in each of the framework regions of cH36 LC was

25   compared with the amino acid sequence in the FRs in human IgG kappa light chain variable domain in Kabat Database. The best-fit FR was selected based on the three criteria described above.

The amino acid sequence of human IgG kappa light chain variable domain

30   with a Kabat Database ID No. 005191 was selected for humanization of cH36 LC

FR1. The amino acid sequence of human IgG kappa light chain variable domain with a Kabat Database ID No. 019308 was selected for humanization of cH36 LC FR2. The following mutations were made in cH36 LC FR1 to match the amino acid sequence of a human IgG kappa light chain variable domain with a Kabat Database

5   ID No. 005191: Q11 → L, L15 → V, E17 → D, S18 → R. One mutation Q37 → L was made cH36 LC FR2 to match the amino acid sequence of a human IgG kappa light chain variable domain with a Kabat Database ID No. 019308 (see Table 1A for sequence information).

10   The amino acid sequence of a human IgG kappa light chain variable domain with a Kabat Database ID No. 038233 was selected for humanization of cH36 LC FR3. The amino acid sequence of a human IgG kappa light chain variable domain with a Kabat Database ID No. 004733 was selected for humanization of cH36 LC FR4. The following mutations were made in cH36 LC FR3 to match the amino acid

15 sequence of a human IgG kappa light chain variable region with a Kabat Database ID No. 038233: K70 → D, K74 → T, A80 → P, V84 → A, N85 → T. Two mutations A100 → Q and L106 → I were made cH36 LC FR4 to match the amino acid sequence of a human IgG kappa light chain variable domain with a Kabat Database ID No. 004733 (see Table 1B for sequence information).

20

     B(ii). Selection of Human IgG Heavy Chain Variable Domain Framework Regions

     The amino acid sequence in each of the framework regions of cH36 HC was
25 compared with the amino acid sequence in the FRs in human IgG heavy chain variable domain in Kabat Database. The best-fit FR was selected based on the three criteria described above.

     The amino acid sequence of a human IgG heavy chain variable domain with a
30 Kabat Database ID No. 000042 was selected for humanization of cH36 HC FR1. The amino acid sequence of a human IgG heavy chain variable domain with a Kabat

40

Database ID No. 023960 was selected for humanization of cH36 HC FR2. The following mutations were made in cH36 HC FR1 to match the amino acid sequence of a human IgG heavy chain variable domain with a Kabat Database ID No. 000042: E1 → Q, Q5 → V, P9 → G, L11 → V, V12 → K, Q19 → R, T24 → A. Two

5   mutations H41 → P and S44 → G were made cH36 HC FR2 to match the amino acid sequence of a human IgG heavy chain variable domain with a Kabat Database ID No. 023960 (see Table 2A for sequence information).

The amino acid sequence of a human IgG heavy chain variable domain with a

10   Kabat Database ID No. 037010 was selected for humanization of cH36 HC FR3. The amino acid sequence of a human IgG heavy chain variable domain with a Kabat Database ID No. 000049 was selected for humanization of cH36 HC FR4. The following mutations were made in cH36 HC FR3 to match the amino acid sequence of a human IgG heavy chain variable domain with a Kabat Database ID No. 037010:

15   S76 → T, T77 → S, F80 → Y, H82 → E, N84 → S, T87 → R, D89 → E, S91 → T. One mutations L113 → V was made cH36 HC FR2 to match the amino acid sequence of a human IgG heavy chain variable domain with a Kabat Database ID No. 000049 (see Table 2B for sequence information).

Table 1. Comparison of cH36 and Human Light Chain (LC) FR Sequences

Table 1A

Names	LC-FR1 (23 aa)	LC-FR2 (15 aa)
cH36-LC	1 10 20 DIQMTQSPASQSASLGESVTITC	35 49 WYQQKPGKSPQLLIY
Human-LC	L V DR 005191	L 019308

Table 1B

Names	LC-FR3 (32 aa)	LC-FR4 (10 aa)
cH36-LC	57 60 70 80 88 98 107 GVPSRFSGSGSGTKFSFKISSLQAEDFVNYYC	FGAGTKLELK
Human-LC	D T P AT 038233	Q I 004733

Table 2. Comparison of cH36 and Human Heavy Chain (HC) FR Sequences

Table 2A

Names	HC-FR1 (30 aa)	HC-FR2 (14 aa)
cH36-HC	1 10 20 30 36 EIQLQQSGPELVKPGASVQVSCKTSGYSFT WVRQSHGKSLEWIG	
Human-HC	Q V G VK R A P G 000042	023960

Table 2B

Names	HC-FR3 (32 aa)	HC-FR4 (11 aa)
cH36-HC	67 75 85 95 107 117 KATLTVDKSSTTAFMHLNSLTSDDSAVYFCAR	WGQGTTLTVSS
Human-HC	TS Y E S R E T 037010	V 000049

Once the decisions on the desired human framework regions were made, the following three techniques were used to achieve the desired amino acid substitutions in both the light and heavy chains: (1) Regular PCR was used for cloning, to introduce cloning or diagnostic restriction endonuclease sites, and to change amino acid residues located at the ends of the variable domains. (2) PCR-based mutagenesis

was used to change multiple amino acid residues at a time, especially when these residues were in the middle of the variable domains. (3) Site-directed mutagenesis was used to introduce one or two amino acid substitutions at a time. Site-directed mutagenesis was done following the protocol described in Stratagene's

5   "QuickChange Site-Directed Mutagenesis Kit" (Catalog #200518).

After each step, the partially humanized clones were sequenced and some of these variable domains were later cloned into expression vectors. The plasmid tKMC180 was used to express LC mutants, and the pJRS 355 or pLAM 356 vector

10   was used to express HC mutants as IgG1 or IgG4, respectively. Some of these clones were then combined and expressed transiently in COS cells to determine the expression levels by ELISA.

The final fully humanized forms of the anti-TF heavy and light variable

15   domains were cloned into what is sometimes referred to herein as a "mega vector" and transfected into CHO and NSO cells for IgG expression. Stable cell lines were then used to produce amounts of humanized anti-TF sufficient for analysis. The resulting humanized versions are 100% human in origin (when the CDR sequences are not considered). The humanized IgG4 kappa version is designated hFAT

20   (humanized IgG Four Anti-Tissue Factor antibody) and the IgG1 kappa version is designated hOAT (humanized IgG One Anti-Tissue Factor antibody). These fully humanized versions of cH36 are intended for treating chronic indications, such as thrombosis, cancer and inflammatory diseases.

25   C. Generation of Humanized Anti-TF Antibody Heavy Chain

1. PCR amplification and cloning into pGem T-easy of anti-TF mAb cH36 heavy chain (HC) variable domain were performed using plasmid pJAIgG4TF.A8 (an expression vector for chimeric H36) as template and

30   primers TFHC1s2 and TFHC1as2. Primer TFHC1s2 introduced a *BsiW*1 site upstream of the initiation codon and also an amino acid change E1 to Q in

framework (FR) 1. Primer TFHC1as introduced an amino acid change **L113** to V in FR4. This step resulted in the construct **HC01**.

2. PCR-based mutagenesis using the previous construct (HC01) and the following four primers generated construct **HC02**. Upstream PCR used primers TFHC1s2 and TFHC7as. Downstream PCR used primers TFHC7s and TFHC1as2. PCR using upstream and downstream PCR products as templates and with primers TFHC1s2 and TFHC1as2 yielded **HC02**. The use of primers TFHC7s and TFHC7as introduced two amino acid changes in FR2: **H41** to P and **S44** to G.

3. PCR-based mutagenesis using HC02 as template and the following four primers generated construct **HC03**. Upstream PCR used primers TFHC1s2 and TFHC5as2. Downstream PCR used primers TFHC5s and TFHC1as2. PCR using upstream and downstream PCR products as templates and with primers TFHC1s2 and TFHC1as2 yielded **HC03**. The use of primers TFHC5s and TFHC5as2 introduced three amino acid changes in FR3: **T87** to R, **D89** to E, and **S91** to T. A *Bgl* II site was also introduced at position. 87.

4. PCR amplification was performed using primers TFHC2s and TFHC3as and HC03 in pGem as template. TFHC2s sits upstream of the cloning site in pGem. TFHC3as sits in framework 3 and introduces two amino acid changes in FR3: **H82** to E and **N84** to S. The resulting PCR band was cloned into pGem and then the proper size insert was digested with *BsiW*1 and *Bgl* II. Cloning of this fragment into **HC03** yields **HC04**.

5. PCR-based mutagenesis using **HC04** as template and the following primers resulted in **HC05**. Upstream PCR used primers TFHC1s2 and TFHC6as. Downstream PCR used primers TFHC6s and TFHC1as2. Mutagenic PCR using upstream and downstream PCR products as templates and with primers

TFHC1s2 and TFHC1as2 yielded **HC05**. This step introduced the following amino acid changes in FR3: **S76** to T, **T77** to S, and **F80** toY.

6. PCR-based mutagenesis using **HC05** as template and the following four
primers generated **HC06**. Upstream PCR used primers TFHC2s and
TFHC2as2. Downstream PCR used primers TFHC3s2 and TFHC1as2.
Amplification using TFHC2as2 introduced an amino acid change in FR1: **P9**
to G. Primer TFHC3s2 changes **Q19** to R and **T24** to A. PCR using
upstream and downstream PCR products as template and with primers
TFHC1s2 and TFHC1as2 yielded **HC06.**

7. A point mutation from I to M in position 2 of FR1 was spontaneously
introduced during construction of **HC06**. PCR amplification using **HC06** as
template and TFHC1s3 and TFHC1as2 as primers, corrected this erroneous
substitution and also introduced an amino acid. change in FR1: **Q5** to V. The
resulting construct was **HC07**.

8. Construct **HC08** was made by PCR-based mutagenesis using **HC07** as
template and the following primers. TFHC2s and TFHC2as3 were used for
the upstream product. The downstream product was previously amplified
using TFHC1s3 and TFHC1as2 (see step 7). The use of primer TFHC2as3
introduced two amino acid changes in FR1: **L11** to V and **V12** to K. A
spontaneous point mutation resulted in a phenylalanine to leucine (F → L)
change at position 64 in CDR2. Further screening and sequencing yielded
construct **HC08R1**, which has the correct sequence of F at position 64 in
CDR2.

9. Two constructs, **HC11** and **HC12**, were generated by site-directed
mutagenesis from **HC07**. Two complementary primers TFHC8sP and
TFHC8asP were used along with **HC07** as template to produce **HC11** which
contains three amino acid changes in FR1: G9 to P, L11 to V, and V12 to K.

45

Then, **HC11** was methylated and column purified for the next round of site directed mutagenesis. PCR using **HC11** as a template and the complementary primers TFHC9sL and TFHC0asL generated **HC12** which has a mutation from **V11** to L in FR1.

5

     10. Construct **HC09** was derived from **HC12** by performing PCR using **HC12** as a template and the complementary primers TFHC10sK and TFHC10asK. **HC09** contains an amino acid change: **K12** to V in FR1.

10   11. Construct **HC10** was made from **HC09**. PCR using **HC09** as a template and the complementary primers LV-1 and LV-2 resulted in the generation of **HC10**, which contains a mutation from **L11** to V in FR1.

After each mutation step, the partially humanized or fully humanized clones were

15 sequenced and some of these variable domains were later cloned into expression vectors. pJRS 355 or pLAM 356 vector was used to express HC mutants fused to Fc of human IgG1 or IgG4.

Figures 3A-D summarize steps 1-11 and shows incremental amino acid changes

20 introduced into FR1-4. Except HC08, all other heavy chain mutants and cH36 contain F at position 64 in CDR2. HC08 has a mutation from F to L at position 64. Figures 4B-D show the heavy chain CDR sequences.

Primers Used for Heavy Chain Humanization

25

TFHC1s2
5' TTTCGTACGTCTTGTCCCAGATCCAGCTGCAGCAGTC 3'

TFHC1as2
30 5' AGCGAATTCTGAGGAGACTGTGACAGTGGTGCCTTGGCCCCAG 3'

TFHC7s
5' GTGAGGCAGAGCCCTGGAAAGGGCCTTGAGTGGATTGG 3'

35 TFHC7as

5' CCAATCCACTCAAGGCCCTTTCCAGGGCTCTGCCTCAC 3'

TFHC5s
5'GCATCTCAACAGCCTGAGATCTGAAGACACTGCAGTTTATTTCTGTG 3'

5

TFHC5as2
5' CTGCAGTGTCTTCAGATCTCAGGCTGTTGAGATGCATGAAGGC 3'

TFHC3as
10   5' GTCTTCAGATCTCAGGCTGCTGAGCTCCATGAAGGCTGTGGTG 3'

TFHC2s
5' TACGACTCACTATAGGGCGAATTGG 3'

15   TFHC6s
5' CTGTTGACAAGTCTACCAGCACAGCCTACATGGAGCTCAGCAG 3'

TFHC6as
5' CTGCTGAGCTCCATGTAGGCTGTGCTGGTAGACTTGTCAACAG 3'

20
TFHC2as2
5' GCACTGAAGCCCCAGGCTTCACCAGCTCACCTCCAGACTGCTGCAGC 3'

TFHC3s2
25   5'CTGGGGCTTCAGTGCGGGTATCCTGCAAGGCTTCTGGTTACTCATTCAC
3'

TFHC1s3
5' TCGTACGTCTTGTCCCAGATCCAGCTGGTGCAGTCTGGAGGTGAGC 3'

30
TFHC2as3
5' GCACTGAAGCCCCAGGCTTCTTCACCTCACCTCCAGACTGCACC 3'

TFHC9sL
35   5' GCAGTCTGGACCTGAGCTGAAGAAGCCTGGGG 3'

TFHC9asL
5' CCCCAGGCTTCTTCAGCTCAGGTCCAGACTGC 3'

40   TFHC8sP
5' GCTGGTGCAGTCTGGACCTGAGGTGAAGAAGCC 3'

TFHC8asP
5' GGCTTCTTCACCTCAGGTCCAGACTGCACCAGC3'

45
TFHC10sK

47

5' GCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTC 3'

TFHC10asK
5' GAAGCCCCAGGCTTCACCAGCTCAGGTCCAGACTGC 3'

5

LV-1
5' CAGTCTGGACCTGAGGTGGTGAAGCCTGGG 3'

LV-2
10   5' CCCAGGCTTCACCACCTCAGGTCCAGACTG 3'

D.   Generation of Humanized Anti-TF Antibody Light Chain

15   1. PCR amplification was performed using plasmid pJAIgG4TF.A8 (an expression
          vector for chimeric H36) as template and primers TFLC1s2.1 and TFLC1as2.
          This step introduced a cloning site, *Age*I, upstream of the coding region. It also
          introduced the **L106I** mutation in FR4. This step yielded the construct **LC03**.

20   2. Site-directed mutagenesis was performed using complementary primers TFLC5s
          and TFLC5as and LC03 as template. This step introduced the mutation **Q37L** in
          FR2 and added a *Pst*I site for diagnostic purposes. This new construct is named
          LC04.

25   3. PCR amplification was performed using **LC04** as template and primers TFHC2s
          and TFLC2as1. This step generated **Fragment A** that will be used in step 6. This
          step introduced **Q11L** and **L15V** mutations in FR1.

      4. PCR amplification was performed using **LC04** as template and primers
30   TFLC1s2.1 and TFLC1asR. This introduced the *Kpn*I site at the end of LC
          variable domain. Cloning of this PCR fragment into pGEM yields **pGEM04K**
          that will be used in step 6.

      5. PCR amplification was performed using **LC04** as template and primers TFLC2s
35   and TFLC4as. This step generated **Fragment C** that will be used in step 6.

Three mutations **E17D, S18R** in FR1 and **A100Q** in FR4 were introduced in this step.

6. PCR-based mutagenesis using **Fragment A** and **Fragment C** as templates and primers TFHC2s and TFLC4as yielded **Fragment D**. Cloning of **Fragment D** into pGEM04K yielded the construct **LC05**.

7. PCR amplification was performed using pGEM04K as template and primers TFLC1s2.1 and TFLC4as. This step generated **Fragment H**, which is then cloned into pGEM04K. This introduced the **A100Q** mutation in FR4 and the construct is named **LC06**.

8. PCR amplification was performed using **LC06** as template and primers TFLC1s2.1 and TFLC3as. This step generated **Fragment I** that will be used in step 10. This introduced the **K70D** and the **K74T** mutations in FR3.

9. PCR amplification was performed using **LC06** as template and primers TFLC3s2 and TFLC4as. This step generated **Fragment F** that will be used in step 10. This introduced the **A80P** mutation in FR3.

10. PCR using **Fragment I** and **Fragment F** as templates and primers TFLC1s2.1 and TFLC4as yielded **Fragment J**. Cloning of **Fragment J** into pGEM yielded the construct **LC07**.

11. Site-directed mutagenesis was conduced using complementary primers TFLC08sds and TFLC08sdsa and **LC07** as template. This step introduced the mutations **V84A** and **N85T** in FR3. This construct is named **LC08**.

12. The *Age*I to *Eco*O109I fragment from **LC05** containing the mutations **Q11L, L15V, E17D, S18R** and **Q37L** is cloned into **LC08**. This yielded the construct **LC09**.

13. Site-directed mutagenesis was conduced using **LC09** as template and the complementary primers LC105 and LC103. This step introduced the **T85N** mutation in FR3 and yielded the construct **LC10**.

14. Site-directed mutagenesis was conducted using **LC10** as template and the complementary primers LC115 and LC113. This step introduced the **D70K** mutation in FR3. This yielded the construct **LC11**.

15. Site-directed mutagenesis was conducted using **LC11** as template and the complementary primers LC125a and LC123a. This step introduced the **K42Q** mutation in FR2. This yielded the construct **LC12**.

After each mutation step, the partially humanized or fully humanized LC clones were sequenced and some of these variable domains were later cloned into expression vector tKMC180.

Oligonucleotide Primers Used for Light Chain Humanization

TFLC1as2:
5' TTCGAAAAGTGTACTTACGTTTGATCTCCAGCTTGGTCCCAG 3'

TFLC1s2.1:
5' ACCGGTGATATCCAGATGACCCAGTCTCC 3'

TFLC5s:
5' GGTTAGCATGGTATCTGCAGAAACCAGGG 3'

TFLC5as:
5' CCCTGGTTTCTGCAGATACCATGCTAACC 3'

TFHC2s:
5' TACGACTCACTATAGGGCGAATTGG 3'

TFLC2as1:
5' CCACAGATGCAGACAGGGAGGCAGGAGACTG 3'

TFLC1asR:

5'
TTCGAAAAGTGTACTTACGTTTGATCTCCAGCTTGGTACCAGCACCGAAC
G 3'

5

TFLC2s:

5' CCTGTCTGCATCTGTGGGAGATAGGGTCACCATCACATGC 3'

TFLC4as:

10   5' GATCTCCAGCTTGGTACCCTGACCGAACGTGAATGG 3'

TFLC3as:

5' GTAGGCTGCTGATCGTGAAAGAAAGTCTGTGCCAGATCC 3'

15   TFLC3s2:

5' CACGATCAGCAGCCTACAGCCTGAAGATTTTGTAAATTATTACTGTC 3'

TFLC08sds:

5' GCAGCCTACAGCCTGAAGATTTTGCAACTTATTACTGTCAACAAG 3'

20

TFLC08sdsa:

5' CTTGTTGACAGTAATAAGTTGCAAAATCTTCAGGCTGTAGGCTGC 3'

LC105:

25   5' CAGCAGCCTACAGCCTGAAGATTTTGCAAATTATTACTGTCAAC 3'

LC103:

5' GTTGACAGTAATAATTTGCAAAATCTTCAGGCTGTAGGCTGCTG 3'

30   LC115:

5' CAGTGGATCTGGCACAAAGTTTTCTTTCACGATCAGCAGC 3'

LC113:

5' GCTGCTGATCGTGAAAGAAAACTTTGTGCCAGATCCACTG 3'

35

LC125a:

5' CTGCAGAACCAGGGCAATCTCCTCAGCTCCTG 3'

LC123a:

40   5' CAGGAGCTGAGGAGATTGCCCTGGTTTCTGCAG 3'

Figure 5A shows the sequence of the human kappa light chain constant
domain (SEQ ID NO. _____). Figure 5B shows the human IgG1 heavy chain

constant domain (SEQ ID NO. ___). Figure 6A shows the hFAT (IgG4) constant

domain sequence (SEQ ID NO. ____). Figure 6B provides the human IgG4 heavy

chain constant domain (SEQ ID NO. ___). See also the published U.S. patent

application number 20030190705 and references cited therein for additional

5   disclosure relating to the foregoing immunoglobulin constant domain sequences.

EXAMPLE 2 – Expression and Purification of Humanized anti-TF Antibodies

10   The partially humanized or fully humanized LC and HC clones were cloned

into expression vectors. The plasmid tKMC18 was used to express LC mutants fused

to human kappa chain, and pJRS 355 or pLAM 356 vector was used to express HC

mutants fused to Fc of human IgG1 or IgG4. Some combinations of the HC and LC

clones were then co-transfected into COS cells. The transiently expressed IgGs in

15   COS cells were assayed for the whole IgG production and binding to TF by ELISA.

For disclosure relating to these particular vectors see the published U.S. patent

application number 20030190705 and references cited therein.

The final fully humanized forms of the anti-TF heavy and light variable

20   domains (combination of HC08 and LC09) were cloned into what is referred to as a

Mega expression vector (pSUN34, see Figure 2) and transfected into CHO and NSO

cells for IgG expression. Stably transfected cell lines producing the IgG4κ or IgG1κ

humanized anti-TF antibody were cloned. The selected stable cell lines were then

used to produce amounts of humanized anti-TF sufficient for analysis. The resulting

25   humanized versions are approximately 100% human in origin (when the CDR

sequences are not considered). The humanized IgG4 kappa version (produced by

pSUN35) is designated hFAT (humanized IgG Four Anti-Tissue Factor antibody) and

the IgG1 kappa version (produced by pSUN34) is designated hOAT (humanized IgG

One Anti-Tissue Factor antibody). These fully humanized versions of cH36 are

30   intended for treating chronic indications, such as cancer and inflammatory diseases.

One of the NSO cell lines (OAT-NSO-P10A7) that expresses (combination of HC08 and LC09) was thawed and extended in 10 mL of IMDM medium supplemented with 10% FBS in a 15 mL tube and centrifuged. The cell pellet was resuspended in 10 mL of fresh media and passed to a T25 flask and incubated at 37°C

5   in 5% CO_2. In order to prepare a sufficient number of cells to inoculate a hollow fiber bioreactor, the cells were expanded to obtain a total of $6x10^8$ cells. A bioreactor was set up as per manufacturer's instruction manual. The harvested cells were pelleted and resuspended in 60 mL of IMDM containing 35% FBS and injected into the extracapillary space of the bioreactor. Concentrations of glucose and lactate were

10   monitored daily and the harvest material was centrifuged and pooled. The harvested material was tested for anti-TF antibody concentrations by ELISA assay. The pooled sample containing anti-TF antibody (hFAT) were then purified and analyzed as described below.

15   A. rProtein A Sepharose Fast Flow Chromatography

Recombinant humanized anti-TF monoclonal antibody consists of two light and two heavy chains. Heavy chain is a fusion of mouse variable domain (unaltered or humanized as described above) and human IgG1 or IgG4 Fc domain, while light

20   chain contains mouse variable domain (unaltered or humanized as described above) and human κ domain. It is well established that human IgG Fc region has high affinity for Protein A or recombinant Protein A (rProtein A).

Harvest pools containing humanized anti-TF antibody (hFAT) were adjusted

25   to pH 8.0 ± 0.1 by adding 0.08 ml of 1 M Tris-HCl, pH 8.0 per ml of sample. Then the sample is filtered through low protein-binding 0.22 micron filters (e.g., Nalgene sterile disposable tissue culture filter units with polyethersulfone membrane from Nalge Nunc International, Cat. No. 167-0020). Following sample application, rProtein A column (from Pharmacia) is washed with 5 bed volumes of 20 mM Tris-

30   HCl, pH 8.0 to remove unbound materials such as media proteins. Since the harvest medium contains high content of bovine serum, a stepwise pH gradient wash was

used to remove bovine IgG from the column. The stepwise pH gradient was achieved by increasing the relative percentage of Buffer B (100 mM acetic acid) in Buffer A (100 mM sodium acetate). A typical pH stepwise wash employed 20%, 40%, and 60% Buffer B. Elute the column with 100% Buffer B and collect fractions based on

5   A_{280}. The pooled fractions were adjusted to pH 8.5 with addition of 1 M Tris base.

B. Q Sepharose Fast Flow Chromatography

Anion ion exchange chromatography is very effective in separating proteins

10   according to their charges. The eluted and pH-adjusted sample from rProtein A column was diluted with two volumes of water, and the pH is checked and adjusted to 8.5. The sample was then loaded to a 5 ml (1.6 x 2.5 cm) Q Sepharose Fast Flow equilibrated with 20 mM Tris-HCl, pH 8.5 and the column washed with (1) 5 bed volumes of 20 mM Tris-HCl, pH 8.5; and (2) 4 bed volumes of 20 mM Tris-HCl, pH

15   8.5 containing 100 mM NaCl. The IgG protein was then eluted with bed volumes of 20 mM Tris-HCl, pH 8.5 containing 500 mM NaCl. The protein peaks were pooled and buffer-exchanged into PBS using ultrafiltration device.

20   **EXAMPLE 3**: Septic Shock Model in Rhesus Monkeys

In this model, septic shock was induced by infusion of live *E. coli*, a gram-negative bacterium (see Taylor *et al.*, J. Clin. Invest. **79**:918-825 (1987)) in rhesus monkeys. The shock induced by *E. coli* causes activation both coagulation and

25   inflammation, ultimately leading to death. The ability of an anti-TF antibody of the present invention to prolong the survival times of rhesus monkeys treated with live *E. coli* was examined using the rhesus model of septic shock described by Taylor *et al.*, *supra*. Rhesus monkeys weighing 3-5 kilograms were fasted overnight before study and immobilized the morning of the experiment with ketamine hydrochloride (14

30   mg/kg, intramuscularly). Sodium pentobarbital was then administered in the cephalic vein through a percutaneous catheter to maintain a light level of surgical anesthesia (2 mg/kg initially and with additional amounts approximately every 20 to 45 minutes for

6 hours). A femoral vein was exposed aseptically and cannulated in one hind limb for sampling blood and administering gentamicin. Gentamicin was administrated by means of 30-minute intravenous infusions. An infusion of 9 mg/kg was administrated at the end of *E. coli* infusion (t = 2 hours). An infusion of 4.5 mg/kg

5   was administrated 6 hours after *E. coli* infusion. Additional gentamicin (4.5 mg/kg, i.m.) was administrated once daily after day 1 for 3 more days. Each monkey was placed on its side in contact with controlled-temperature heating pads and rectal temperature was monitored. Animals were intubated orally and allowed to breathe spontaneously.

10

The *E. coli* strain 086:K61H (ATCC 33985) was freshly prepared in less than 12 hours prior to injection. Each monkey received a 2-hour intravenous infusion of *E. coli* at a dose of 4×10^{10} CFU/kg. Control group monkeys received PBS 30 minutes before infusion of *E. coli*. Treatment group monkeys received a bolus (2-3

15   minutes) dose of anti-tissue factor antibody (cH36, diluted in PBS if necessary) 30 minutes before infusion of *E. coli* (see Timeline for injection schedule). The percutaneous catheter was used to infuse *E. coli*, PBS and anti-TF antibody.

Timeline for anti-TF antibody and *E. coli* administration.

All monkeys were monitored continuously for 8 hours and observed daily for a maximum of 7 days, for the following: survival time: monitored and recorded hourly; temperature was measured and recorded hourly for the first 8 hours and then once a day for up to 7 days.

Blood samples were collected at the following time points: T = -0.5*, 0**, 1, 2, 4, 6, 24 hours as shown in Table 3 for the analysis of hematological references and inflammatory cytokines. (*T = -0.5, right before injection of cH36 or saline control; **T = 0, right before infusion of *E coli* but 30 min after injection of cH36 or saline control).

Table 3. The schedule for collecting blood samples.

Time Point	Hematology	Plasma for Analysis
Day 1; t = -0.5 hr (just prior to test article or vehicle infusion)	X	X
Day 1; t = 0 hour (30 minutes after treatment, just prior to E. coli infusion)	X	X
Day 1; 1 hour (following E. coli infusion	X	X
Day 1; 2 hour (following E. coli infusion)	X	X
Day 1; 4 hour (following E. coli infusion)	X	X
Day 1; 6 hour (following E. coli infusion)	X	X
Day 1; 24 hour (following E. coli infusion)	X	X
Volume of whole blood / time point	1.0 mL	1.8 mL
Anticoagulant	EDTA	Sodium Citrate

The results of this study are shown in Table 4 and Fig.7A-D. Anti-TF antibody cH36 protected rhesus monkeys very well from E. coli-induced septic shock when administered as a10 mg/kg bolus injected intravenously (Table 4), while attenuating inflammatory cytokines IL-8 and IL-1β, and to a lesser extent IL-6 and TNF-α (Fig. 7A-D).

Table 4. Protective Effect of cH36 on E coli-induced Septic Shock in Rhesus Monkeys

Treatment	Weight (kg)	Sex	Survival Time (hr)	Average Survival Time (hr)
Saline	3.6	F	8	
	4.5	M	24	16
Sunol-cH36 (10 mg/kg)	3.1	F	>168	
	4.0	M	54	>111

EXAMPLE 4: Acute Lung Injury Model in Baboons

A. Acute lung injury is an important cause of morbidity and mortality in sepsis. Patients infected with gram-negative sepsis have a high incidence of acute respiratory distress syndrome and multiple organ failure. It has been shown that blocking tissue factor function with active site-inactivated factor VIIa could limit

sepsis-induced acute lung injury and other organ damage in baboons (see Welty-Wolf, K. *et al.*, *Am. J. Respir. Crit. Care Med.* 164:1988 (2001)). A critical pathophysiological feature of the acute respiratory distress syndrome (ARDS) is local activation of extrinsic coagulation and inhibition of fibrinolysis. As the injury

5   evolves, these perturbations cause deposition of fibrin in the microvascular, interstitial and alveolar spaces of the lung leading to capillary obliteration and hyaline membrane formation. Components of the extrinsic coagulation pathway such as TF, thrombin and fibrin signal alterations in inflammatory cell traffic and increases in vascular permeability. Procoagulants and fibrin also promote other key events in the

10   injury including complement activation, production of proinflammatory cytokines, inhibition of fibrinolysis, and remodeling of the injured lung. It has been established that sepsis-induced TF expression activates the extrinsic coagulation cascade in the lung and leads to a procoagulant environment, which results in fibrin deposition and potentiates inflammation. By blockade of the initiating events of extrinsic

15   coagulation, their effects on proinflammatory events in the lungs and disordered fibrin turnover may be corrected and the evolution of severe structural and functional injury may be averted during experimental ARDS. Recent studies demonstrated that preventing initiation of coagulation at TF-Factor VIIa complex with active site inhibited factor VIIa (FVIIai) or TF pathway inhibitor (TFPI) attenuates fibrin

20   deposition and inflammation in sepsis, thereby limiting acute lung injury (ALI) and other organ damage in baboons.

A model for sepsis-induced ALI model has been established in baboons. See Welty-Wolf, K. *et al.*, *Am. J. Respir. Crit. Care Med.* 164:1988 (2001). In this

25   model, hyperdynamic cardiovascular and systemic inflammatory responses are pre-activated by a priming infusion of killed *E. coli*. After 12 hours, a second dose of live *E. coli* is given to the animals to induce pulmonary and renal failure similar to humans with sepsis and ARDS. Using this model, blockade of TF function by FVIIai and TFPI was shown to attenuate systemic inflammatory responses, decrease fibrin

30   deposition in tissues, and prevented lung and renal injury.

In this model, overnight fasted, adult baboons (*Papio cyanocephalus*) were sedated with intramuscular ketamine (20-25 mg/kg) and intubated. Heavy sedation was maintained with ketamine (3-10 mg/kg/h) and diazepam (0.4-0.8 mg/kg every 2 hours). Animals were mechanically ventilated (21% O_2) with a volume-cycled

5   ventilator and paralyzed intermittently with pancuronium (4 mg intravenously) before respiratory measurements. An indwelling arterial line and a pulmonary artery catheter were placed via femoral cut down for hemodynamic monitoring. All animals received approximately 10^9 CFU/kg heat-killed *E. coli* 086:K61H (ATCC 33985) as a 60 min infusion at t = 0 h, 12 h before live *E. coli*. Sepsis was induced at t = 12 h by

10   infusing 10^{10} CFU/kg of live *E. coli* in a volume of 50 mL over 60 min. Gentamicin (3 mg/kg i.v.) and Ceftazidime (1 gm i.v.) were administered 60 min after completion of the live *E. coli* infusion. Fluids were given as needed to maintain pulmonary capillary wedge pressure (PCWP) at 8-12 mmHg and to support blood pressure. Dopamine was used for hypotension when mean arterial pressure (MAP) fell below

15   65 mmHg despite fluids. After 48 h (36 h after the live bacteria infusion) animals were deeply anesthetized and killed by KCl injection. Physiologic parameters including heart rate (HR), temperature, arterial blood pressure, pulmonary artery pressure, ventilator parameters, and fluid intake were recorded every hour. Measurements were obtained every six hours of cardiac output (CO) by

20   thermodilution, central venous pressure (CVP), PCWP, arterial and mixed venous blood gases, oxygen saturation, oxygen content and hemoglobin (Hgb) as reported. Urinary catheter output was measured every six hours and fluid balance calculated as total i.v. fluid intake minus urine output.

25   Treatment efficacy for each intervention were assessed by comparing the responses of drug-treated animals with vehicle-treated animals using the physiological, histologic, and biochemical endpoints of lung injury listed below:

•   Physiological endpoints were evaluated as the alveolar-to-arterial O_2 difference ($AaDo_2$), pulmonary system compliance (C_L), pulmonary artery pressures,

30   pulmonary vascular resistance (PVR) and tissue W/D ratios. Secondary

endpoints were fluid volume requirements, serum HCO_3, V_E at constant $PaCO_2$, urine output, creatinine, and systemic DO_2, VO_2 and VCO_2.

- Pathologic endpoints analyzed were gross tissue appearance and qualitative light microscopic analysis, including fibrin deposition, in lung, kidney, adrenal, and other tissues.

- Biochemical endpoints were tissue myeloperoxidase (MPO) levels, total tissue and lavage protein, and lavage LDH. Lung and small bowel edema were measured by wet/dry weights.

Blood samples were drawn at 0, 12, 13, 18, 24, 36, and 48 h. Plasma (from citrated blood) and serum were separated and stored at -80° C. Plasma samples were assayed for interleukin (IL) 6 and IL 8 using ELISA kits (R and D Systems, Inc., Minneapolis, MN).

The experimental protocol is summarized in Table 5.

Table 5. Experimental Protocol

Time (hours)	0	6	12	14	18	24	30	36	42	48		
Heat-killed *E. coli*	X											
Live *E. coli*			X									
Antibiotics				X								
Vehicle or drug				X	X	X	X	X	X	X		
Studies*	X	X	X	X	X	X	X	X	X	X		
Sacrifice										X		
*Studies include serum, plasma, urine and physiology measurements outlined in the detailed methods.												

TF blockade was done using a total antibody dose of 3.5 mg/kg for the cH36 Fab and 5.25 mg/kg for cH36. The intravenous loading dose of test article (1.8 mg/kg for cH36 Fab or 2.7 mg/kg for cH36) was begun 2 hours after infusion of live microorganisms, at the time antibiotics were administered, followed by a constant 34-hour infusion of 50 mcg/kg per hour for cH36 Fab or 75 mcg/kg/hour for cH36.

Table 6. Experimental Design

Group	Treatment	# Animals
1	Sepsis + vehicle	5
2	Sepsis + cH36 Fab (3.5 mg/kg total, 1.8 mg/kg loading, 50 mcg/kg/hr infusion for 34 hr)	2
3	Sepsis + Sunol-cH36 (5.25 mg/kg total, 2.7 mg/kg loading, 75 mcg/kg/hr infusion for 34 hr)	5

TF blockade with bolus injection of cH36, followed by infusion, attenuated systemic expression of the proinflammatory cytokine IL-8 and IL-6 to a lesser extent (Figs. 11A-B), and provided partial renal and lung protection in baboons challenged with *E. coli*. Interim analysis indicates that cH36 administration attenuates increases in mean pulmonary artery pressure, lung system compliance (Figs. 8A-B) and in the alveolar-arterial oxygen gradient. The kidneys in the animals examined thus far appeared grossly normal at necropsy, the

kidney myeloperoxidase levels remained lower (Figure 9A) and urine output was maintained throughout the experiments. The small bowel wet/dry ratio in the treated animals was significantly lower that in the control animals indicative of less edema in the cH36 treated animals (Figure 9B).

These data indicate that coagulation blockade targeting TF with Sunol-cH36 prevents inflammation and the development of organ injury in gram-negative sepsis. These data also show, for the first time, a new strategy for management of ARDS in humans with anticoagulant.

B. The following data further show that cH36 and cH36-Fab are useful in preventing lung injury in septic baboons.

Briefly, the objective of this part of the example is to further confirm effects of Sunol-cH36 and cH36-Fab on procoagulant-fibrinolytic balance and inflammation in the lung and relate them to the structural and gas exchange abnormalities in ALI in an experimental sepsis model in baboons. See section A, above.

All baboons (*Papio cyanocephalus*) were mechanically ventilated (21% O_2), anesthetized, and given a dose of heat-killed *E. coli* (1 x 10^9 CFU/kg) intravenously 12 hours prior to the onset of live *E. coli* sepsis (1-2 x 10^{10} CFU/kg). The study design consisted of three groups of baboons as shown in Table 7, below. The baboons in the first group (n=6) were administered vehicle (PBS) and served as controls. The animals in the second group (n=3) were injected with cH36-Fab (3.5 mg/kg total, 1.8 mg/kg bolus loading dose followed by constant infusion of 50 mcg/kg/hr for 34 hours). The third group (n=6) received cH36 (5.25 mg/kg total, 2.7 mg/kg bolus loading dose followed by a constant infusion of 75 mcg/kg/hr for 34 hours). The intravenous loading dose of drug (1.8 mg/kg for cH36-Fab or 2.7 mg/kg for cH36) was started 2 hours after infusion of live microorganisms (at the 14-hour time point) followed by a constant infusion of 50 mcg/kg per hour for cH36-Fab or 75 mcg/kg/hour for cH36 until the end of the experiment at 48 hours. Antibiotics were administered at the 14-hour time point. Treatment efficacy was assessed by comparison of the responses of the treated animals with the controls using physiological, histological and biochemical parameters of lung injury.

Table 7.   Experimental Design

Group	Treatment	No. of Baboons
1	Sepsis + vehicle	6
2	Sepsis + cH36-Fab (3.5 mg/kg total, 1.8 mg/kg loading, 50 mcg/kg/hr infusion for 34 hr)	3
3	Sepsis + cH36 (5.25 mg/kg total, 2.7 mg/kg loading, 75 mcg/kg/hr infusion for 34 hr)	6

From the foregoing data, it can be concluded that animals treated with cH36 had a less hyperdynamic systemic response to sepsis.

The following Materials and Methods were used as needed to conduct the experiments in this Example. They were also used elsewhere in this disclosure as indicated .

C. Materials and Methods

Mechanically ventilated (21% O_2), anesthetized baboons (*Papio cyanocephalus*) were given a dose of heat-killed *E. coli* (1 x 10^9 CFU/kg) intravenously 12 hours prior to the onset of live *E. coli* sepsis (1-2 x 10^{10} CFU/kg). The intravenous loading dose of drug (1.8 mg/kg for cH36-Fab or 2.7 mg/kg for cH36) was started 2 hours after infusion of live microorganisms (14 hours), at the time antibiotics were administered, followed by a constant infusion of 50 mcg/kg per hour for cH36-Fab or 75 mcg/kg/hour for cH36. The total antibody dose was 3.5 mg/kg for the cH36-Fab and 5.25 mg/kg for cH36. Treatment was initiated after the onset of gram-negative sepsis because we have previously shown that TF blockade is effective as a rescue strategy. Because initial studies suggested greater efficacy and no harmful effects of whole antibody compared to Fab, comparisons were made between untreated sepsis controls and septic animals treated with cH36 whole antibody. Experimental groups are as shown in Table 7. Statistical analyses used ANOVA for physiologic data and t test or Mann Whitney U for biochemical and BAL data. Data are expressed as mean ± sem and p values are shown.

Animals were handled in accordance with appropriate guidelines. The animals were divided randomly into treatment and sepsis control groups. After an overnight fast, each animal was sedated with intramuscular ketamine (20-25 mg/kg) and intubated. Heavy sedation was maintained with ketamine (3-10 mg/kg/h) and

5   diazepam (0.4-0.8 mg/kg every 2 hours). Animals were ventilated with a volume-cycled ventilator and paralyzed intermittently with pancuronium (4 mg intravenously) before respiratory measurements. The FiO_2 was 0.21, tidal volume 12 ml/kg, positive end-expiratory pressure 2.5 cm H_2O, and a rate adjusted to maintain an arterial PCO_2 of 40 mmHg. An indwelling arterial line and a pulmonary artery catheter were

10 placed via femoral cut down for hemodynamic monitoring. The animals received gentamicin sulfate (3 mg/kg iv) and ceftazidime (1 gm iv) two hours after the start of live *E. coli* infusion (14 hours). The animals were supported with intravenous volume infusion (Ringer's lactate) at a rate sufficient to maintain the pulmonary capillary wedge pressure (PCWP) at 8 to 12 mmHg. Dopamine was used if needed to maintain

15 mean arterial pressure of 60 mmHg. After 48 h (36 h after the live bacteria infusion) animals were deeply anesthetized and killed by KCl injection. Predefined early termination criteria included refractory hypotension (MAP less than 60 mmHg despite dopamine and adequate PCWP), hypoxemia (need for FIO_2 greater than 40%), or refractory metabolic acidosis (pH < 7.10 with normal $PaCO_2$). The

20 experimental protocol was the same as that shown in Table 5, above.

Physiological parameters including heart rate (HR), temperature, arterial blood pressure, pulmonary artery pressure, ventilator parameters, and fluid intake were recorded every hour. Measurements were obtained every six hours of cardiac

25 output (CO) by thermodilution, central venous pressure (CVP), PCWP, arterial and mixed venous blood gases, oxygen saturation, oxygen content and hemoglobin (Hgb). Urinary catheter output was measured every six hours and fluid balance calculated as total iv. fluid intake minus urine output.

30   Blood samples were drawn at 0, 12, 13, 18, 24, 36, and 48 h. Complete blood

counts were performed on whole blood (Sysmex-1000 Hemocytometer; Sysmex, Inc., Long Grove, IL). Plasma (from citrated blood) and serum were separated and stored at –80°C. Fibrinogen was measured using an ST4 mechanical coagulation analyzer (Diagnostica Stago, Parsippany, NJ). Prothrombin time (PT) and activated partial

5   thromboplastin time (aPTT) were measured in duplicate, and antithrombin III (ATIII) activity was measured on an MDA coagulation analyzer (Organon Teknika, Durham, NC) with a chromogenic assay and expressed as % of the kit standard. ELISA was used to measure plasma thrombin-antithrombin (TAT) complexes (Dade Behring, Deerfield, IL) in plasma and BAL. cH36 and cH36-Fab levels in blood and BAL

10   were measured by Sunol Molecular (Miramar, FL). Serum samples were assayed for interleukin 1β (IL-1β), IL-6, IL-8, and TNF receptor-1 (TNFR-1) using ELISA kits (R and D Systems, Inc., Minneapolis, MN). Blood creatinine was measured with standard clinical techniques.

15   Tissues were collected at autopsy as follows: After the experiments the thorax was opened, the left mainstem bronchus ligated, and the left lung removed. BAL was performed on the left upper lobe with 240 mL 0.9% saline. Samples of lung tissue from the left lower lobe were manually inflated and immersed in 4% paraformaldehyde for light microscopy. Four samples were taken at random from the

20   remainder of the left lung for wet/dry weight determination taking care to avoid large vascular and bronchial structures. Additional samples from lung, kidney, liver, small bowel, heart, and adrenal were flash frozen in liquid nitrogen and stored at –80°C. The entire right lung was inflation-fixed for 15 min at 30 cm fixative pressure with 2% glutaraldehyde in 0.85 M Na cacodylate buffer (pH 7.4). Additional tissue from

25   kidney, liver, small bowel, heart, and adrenal was fixed by immersion in 4% paraformaldehye. Four samples of small bowel were selected randomly for wet/dry weight determination.

Myeloperoxidase (MPO) activity and protein concentration of lung

30   homogenates and protein and lactate dehydrogenase (LDH) concentrations of BAL

fluid were measured as described (*Am J Resp Crit Care Med* 1998;157:938). MPO activity was expressed as a change in absorbance/min/g wet weight tissue. LDH values were expressed in units of activity per liter (U/L).

5   An important objective of the following Examples was to determine the effects of cH36 and cH36-Fab on procoagulant-fibrinolytic balance and inflammation in the lung. It was also an objective to correlate these parameters to the structural and gas exchange abnormalities in ALI in an experimental sepsis model in baboons.

10   **D. Results:** Treatment with cH36 prevents fibrinogen depletion in baboons with *E. coli* sepsis.

15   Briefly, cH36 treatment attenuated fibrinogen depletion and TAT complex formation, consistent with inhibition of TF-dependent activation of coagulation. In sepsis controls, fibrinogen decreased to approximately 50% of initial values, but in animals treated with cH36 mean fibrinogen levels did not drop below baseline values (Figure 10A, p<0.01 versus sepsis controls). PT increased in sepsis controls during
20   sepsis due to a progressive coagulopathy, and also increased in treated animals due to pharmacologic effect of the drug infusion. PT and fibrinogen values in the three cH36-Fab treated animals are also shown for comparison. The decreased values in the cH36-Fab compared to whole antibody treated animals suggest that the Fab fragment has a lower affinity for TF (Figure 10A,B). PTT increased in both groups
25   and was not significantly different. TAT complexes increased after infusion of live bacteria in both groups, peaking at 14 h and then decreasing. Peak TAT value was lower and levels decreased more rapidly in animals treated with cH36 (Figure 10D, p<0.01). The difference in TAT complex formation was not due to differences in ATIII levels, as ATIII decreased similarly in the two groups, to 35-40%.of initial
30   values by the end of the experiment.

E. Results: Treatment with Sunol-cH36 attenuates sepsis-induced acute lung injury

cH36 decreased ALI in baboons with established *E. coli* sepsis, attenuating sepsis-induced abnormalities in gas exchange, pulmonary hypertension, and loss of

5   pulmonary system compliance. These physiologic data are shown in Figures 8A-C. Alveolar arterial oxygen gradient ($AaDO_2$, mmHg) increased in both groups after infusion of killed bacteria and progressively worsened in the sepsis control group after the onset of live bacterial sepsis at t = 12 h. Compared to septic control animals, treatment with cH36 prevented progressive deterioration in gas exchange during

10   sepsis (p = 0.001, Figure 8A). One animal in the sepsis control group required supplemental oxygen after the onset of live bacterial sepsis for progressive hypoxemia. One animal in the cH36 treated group also required oxygen, but only from 18-22 hours, during which oxygenation gradually improved and supplemental O_2 was weaned back to room air. At the end of the experiment the $AaDO_2$ in that

15   animal had recovered to initial values measured prior to infusion of heat-killed or live bacteria. Sepsis-induced increase in mean pulmonary artery pressure (PAM, mmHg) was attenuated by cH36 (p < 0.0001 vs. untreated sepsis controls, Fig 8B) but there was no difference in pulmonary vascular resistance, suggesting that this was due to effect on cardiac output in the treated animals. cH36 also prevented the decrease in

20   pulmonary system compliance (Cst in mL/cm H_2O) seen in sepsis control animals (p < 0.01, Fig 8C). The $PaCO_2$ was controlled within the normal range, between 35-45 mmHg in both groups, but was slightly higher in sepsis controls (p=0.03) despite 20% higher minute ventilation (V_E, l/min, p=0.015), suggesting cH36 attenuated sepsis-induced increases in dead space (Table 7).

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At post-mortem, the lungs from sepsis control animals were dense and hemorrhagic. The gross appearance of the lungs from animals treated with cH36 was improved and in some animals appeared the same as lungs from normal uninjured baboons. Lung wet/dry weights were not significantly different in the two groups,

30   6.32 ± 0.66 in septic controls compared to 5.57 ± 0.34 in cH36 treated animals (p = NS, normal reference range is 4.6-5.0). BAL protein and LDH were also not significantly different between the two groups. BAL protein was 1.0 ± 0.3 in septic

controls compared to 1.0± 0.4 in cH36 treated animals, and LDH was 23.9 ± 10.6 in septic controls compared to 10.6 ± 3 in cH36 treated animals. Neutrophil accumulation, as measured by myeloperoxidase (MPO) activity (OD/min/gm wet wt), was decreased over 40% in cH36 treated animals (p=0.07).

Lung histology showed protection in septic animals treated with cH36. The lungs of sepsis control animals had thickened alveolar septae, patchy alveolar edema and hemorrhage, and intra-alveolar inflammatory cell infiltration with macrophages and PMNs. Lungs of treated animals had improved alveolar septal architecture, decreased alveolar PMN infiltration, less alveolar edema, and no alveolar hemorrhage.

EXAMPLE 5: Treatment with cH36 improves renal function and reduces organ injury in sepsis

Materials and methods used to perform the present Example have been desribed previously. See eg., Example 4.

Treatment with cH36 improved renal function in sepsis. Urine output was significantly higher after infusion of live *E. coli* in animals treated with cH36 compared to untreated controls (p < 0.001). This was not due to differences in resuscitation because fluid balance and systemic hemodynamics were similar in the two groups. Blood pH and serum [HCO3⁻] were lower in untreated animals (both p < 0.0001), and values were consistent with mixed metabolic and respiratory acidosis in sepsis controls. Serum creatinine was not different in the two groups at the end of the experiments, and there was variability in the treated group due to one animal that was not protected.

See Figures 13A-C (showing mean urine output (13A), mean blood pH (13B), and serum bicarbonate levels (13C) with control and cH36 antibodies.

Kidneys from untreated animals were swollen and hemorrhagic at post mortem but appeared more normal in cH36 treated animals. H&E stained sections of the

kidneys of untreated animals had patchy to extensive areas of acute tubular necrosis (ATN) and glomerular damage. The kidneys of treated animals, except for a few small foci of ATN, showed normal renal architecture. MPO values were significantly decreased in kidneys from treated animals (p=0.01).

5   Other organ injury was also improved in the cH36 treated animals. Adrenals from untreated animals were swollen and hemorrhagic and small bowel was grossly edematous. In contrast, adrenals and small bowel appeared almost normal in animals treated with cH36. Small bowel wet/dry weights were decreased in septic animals treated with cH36 (6.46 ± 0.62 in Sunol-cH36 treated vs. 9.70 ± 1.05 in untreated

10   sepsis control animals, p = 0.01). Histology confirmed improvement in small bowel edema. Adrenals were also protected from sepsis, with decrease in congestion and hemorrhage, and areas of cellular damage were markedly diminished. In addition to the decreased neutrophil content in the lung and kidney, cH36 treatment significantly decreased PMN content in the liver (p=0.05,), and histology showed decreased injury

15   to hepatocytes.

EXAMPLE 6: cH36 treatment attenuated sepsis-induced anemia

20   Materials and methods used to perform the present Example have been explained above. See eg., Example 4.

Both groups of animals developed neutropenia, thrombocytopenia and anemia after infusion of live *E. coli* (see Table 8, below). Hemoglobin (Hgb) decreased in

25   both groups but was significantly higher in septic animals treated with cH36 (8.1 ± 0.7 versus 10.8 ± 0.8 g/dL at 48 hours, p < 0.0001). Although platelets declined more rapidly in untreated animals (p<0.0001), the clinical significance of this difference is not clear. All animals developed progressive thrombocytopenia after the infusion of live *E. coli* and mean platelet counts were approximately 30,000 or less in both

30   groups at the end of the experiment. WBC reached a nadir of approximately 1,000-1,500 (x $10^3/\mu L$) in both groups two hours after the infusion (t = 14 h) and

progressively increased to baseline levels by the end of the experiment (12,680 ± 2,012 in treated vs. 10,500 ± 1,336 in untreated animals, p = 0.07). Two sepsis control animals developed self-limited hematuria. Most animals in both groups had some blood tinged secretions associated with suctioning at some point in the study, but there was no clinical evidence of significant hemorrhage (i.e. hematuria, hemoptysis, or bleeding from intravenous or arterial catheter sites) in the cH36 treated animals and no severe or life-threatening bleeding complications occurred in either group.

Table 8

Time (h)		0	12	18	24	36	48	p value
Hgb (g/dL)								
	Sepsis	11.2 ± 0.3	10.6 ± 0.3	10.4 ± 0.5	10.4 ± 0.8	8.7 ± 0.8	8.1 ± 0.7	
	cH36	12.1 ± 0.5	11.8 ± 0.4	12.2 ± 0.5	12.4 ± 0.6	10.9 ± 0.8	10.8 ± 0.8	<0.0001
	cH36 Fab	11.7 ± 0.3	11.5 ± 0.5	12.5 ± 0.8	11.4 ± 0.3	11.3 ± 0.4	9.6 ± 0.1	
Platelets								
	Sepsis	194 ± 15	126 ± 12	59 ± 7	33 ± 5	24 ± 5	26 ± 9	
	-cH36	206 ± 15	167 ± 16	110 ± 13	64 ± 12	40 ± 4	30 ± 4	<0.0001
	cH36 Fab	197 ± 8	146 ± 4	87 ± 10	31 ± 5	21 ± 4	25	
HR (beats/min)								
	Sepsis	95 ± 6	116 ± 10	125 ± 9	129 ± 9	125 ± 5	127 ± 16	
	cH36	84 ± 3	101 ± 4	135 ± 13	123 ± 11	105 ± 12	99 ± 9	<0.01
	cH36 Fab	75 ± 7	89 ± 9	107 ± 14	109 ± 9	98 ± 15	98 ± 9	
MAP (mmHg)								
	Sepsis	111 ± 2	104 ± 2	99 ± 9	102 ± 7	79 ± 10	78 ± 13	
	cH36	102 ± 3	93 ± 3	97 ± 5	92 ± 6	78 ± 9	86 ± 5	NS
	cH36 Fab	108 ± 4	85 ± 4	89 ± 9	78 ± 8	89 ± 4	63 ± 4	
CO/kg								
	Sepsis	0.16 ± 0.01	0.20 ± 0.02	0.23 ± 0.04	0.22 ± 0.03	0.22 ± 0.04	0.23 ± 0.02	
	cH36	0.15 ± 0.01	0.18 ± 0.01	0.16 ± 0.02	0.16 ± 0.02	0.15 ± 0.02	0.18 ± 0.01	<0.0001
	cH36 Fab	0.12 ± 0.01	0.14 ± 0.01	0.12 ± 0.01	0.15 ± 0.01	0.14 ± 0.01	0.14 ± 0.02	
D_{O2}/kg								
	Sepsis	23.2 ± 2.2	28.1 ± 3.1	28.6 ± 4.1	26.2 ± 2.0	22.7 ± 24.3	20.1 ± 1.2	
	cH36	23.8 ± 1.8	28.0 ± 1.0	23.8 ± 2.4	24.9 ± 3.5	23.1 ± 2.6	24.6 ± 2.1	NS
	cH36 Fab	18.1 ± 1.6	21.8 ± 2.1	19.5 ± 1.8	20.9 ± 2.7	21.1 ± 1.8	16.4 ± 1.4	
V_{O2}/kg								
	Sepsis	5.4 ± 0.8	6.3 ± 1.4	6.7 ± 0.6	6.8 ± 1.3	5.7 ± 0.6	5.6 ± 0.7	
	cH36	5.6 ± 0.4	6.6 ± 0.2	6.2 ± 0.4	5.6 ± 0.7	6.1 ± 0.6	6.2 ± 0.3	NS
	cH36 Fab	4.0 ± 0.3	4.2 ± 0.2	3.7 ± 0.4	4.6 ± 0.3	3.7 ± 0.2	4.2 ± 0.2	
SVR*kg								
	Sepsis	56602 ± 5459	41539 ± 5049	35290 ± 4941	37788 ± 5675	30713 ± 9152	26161 ± 5750	
	cH36	50833 ± 3782	37936 ± 895	49953 ± 8998	46811 ± 6290	37432 ± 3612	36058 ± 4362	***
	cH36 Fab	69095 ± 2475	43890 ± 5700	52763 ± 7023	39545 ± 7126	46570 ± 5101	32243 ± 8576	
PCWP								
	Sepsis	10 ± 1	11 ± 1	10 ± 1	11 ± 1	12 ± 1	11 ± 1	
	cH36	10 ± 0	10 ± 0	9 ± 1	9 ± 1	11 ± 2	9 ± 1	NS
	cH36 Fab	12 ± 0	14 ± 1	10 ± 1	10 ± 1	11 ± 1	12 ± 2	
V_E								
	Sepsis	3.5 ± 0.3	3.5 ± 0.2	3.8 ± 0.2	4.2 ± 0.2	5.0 ± 0.5	5.1 ± 0.4	
	cH36	3.7 ± 0.1	3.9 ± 0.2	4.0 ± 0.2	4.3 ± 0.2	4.4 ± 0.3	4.3 ± 0.2	=0.015

cH36 (ng/mL)		4.3 ± 0.2	4.4 ± 0.2 15 hr	4.5 ± 0.1	5.0 ± 0.4	6.4 ± 0.8	6.2 ± 0.9
	cH36 Fab						
	cH36	0	49.3 ± 5.5	51.8 ± 3.3	60.2 ± 6.0	53.0 ± 5.6	58.0 ± 8.3
	cH36 Fab	0	±	±	±	±	±

Clinical and histological evaluations are performed to confirm that anti-tissue factor injections inhibited the development of rheumatoid arthritis in these mice.

Referring to the foregoing Examples and discussion, it was found that animals treated with cH36 had a less hyperdynamic systemic response to sepsis. Most systemic hemodynamic measurements, including mean arterial pressure (MAP), PCWP, systemic vascular resistance*kg (SVR*kg), VO_2, and DO_2, were not altered by treatment with cH36 (Table 8). Hypotension responded to IV fluids and dopamine infusion in both groups. Nine of the 12 animals survived until the scheduled termination point of the protocol. Overall, septic animals treated with cH36 were less hyperdynamic, without further increases in cardiac output (CO/kg) after the onset of live bacterial sepsis, and had less tachycardia and higher systemic vascular resistance*kg (SVR*kg) at the end of the experiment (Table 7, for instance). In some instances, treated animals needed dopamine and fluid support as did the untreated controls and MAP and SVR were not detectably different between the two groups. Survival is not intended for use as an endpoint as all animals were sacrificed at the 48 hour time point. Three septic animals were treated with cH36-Fab to assess for differences between whole antibody and Fab fragment. As expected, the whole antibody was often more effective then the Fab fragment.

EXAMPLE 7: Impact of cH36 on pro-inflammatory cytokine levels

Cytokine levels were measured in serum and BAL fluid along lines already described above (eg., Example 5). In the circulation, cH36 treatment attenuated IL-8 ($p < 0.01$, Fig. 12) but had no detectable effect on IL-1β, or TNFR-1. In BAL fluid, cH36 attenuated elevations in IL-6, IL-8 and TNFR-1. BAL cytokine levels are shown in Table 9 below. We also measured soluble thrombomodulin (sTM) and found no differences in treated vs. untreated animals in serum or BAL. The data

show that inhibiting coagulation using Sunol-cH36 to block the FX binding site on TF-FVIIa complex attenuates acute lung injury at least in part through effects on proinflammatory cytokine levels in the alveolar compartment. This could be an effect on local cytokine production and/or leakage of proteins from the circulation across the alveolar epithelium.

Table 9. BAL cytokine levels

	Sepsis control	Sunol-cH36	p value	cH36–Fab
IL-6 (pg/mL)	600 ± 269	506 ± 522	0.05	1159 ± 435
IL-8 (pg/mL)	1081 ± 448	224 ± 176	0.037	1478 ± 755
IL-1β (pg/mL)	6.9 ± 1.5	7.9 ± 3.1	NS	8.5 ± 1.8
TNFR1 (pg/mL)	294 ± 126	107 ± 31	0.09	167 ± 93
sTM (ng/mL)	1.67 ± 0.54	0.9 ± 0.11	NS	2.17 ± 0.72

Certain results from Examples 4-7 can be summarized as follows:

Most systemic hemodynamic measurements, including mean arterial pressure (MAP), oxygen consumption (VO$_2$/kg), and oxygen delivery (DO$_2$/kg), were not altered by treatment with cH36 (Table 8). Mean pulmonary capillary wedge pressure (PCWP) was slightly higher in sepsis control animals (p<0.01) but both groups were within the set parameters of the study. Systemic vascular resistance*kg (SVR*kg) was slightly higher in treated animals (p< 0.05, Table 3). Hypotension responded to IV fluids and dopamine infusion in both groups. Nine of the 12 animals survived until the scheduled termination point of the protocol. Two sepsis control animals died prior to scheduled termination from ALI, with refractory hypoxemia and respiratory acidosis, one at 30 hours and one at 38 hours. One animal in the H36 group was not protected and died at 36 hours of refractory hypotension and metabolic acidosis. In that animal, lack of protection correlated with lower drug levels. Overall, septic animals treated with cH36 were less hyperdynamic, without further increases in cardiac output (CO/kg) after the onset of live bacterial sepsis, and had less tachycardia and higher systemic vascular resistance per kg (SVR*kg) at the end of the experiment (Table 7).

EXAMPLE 8:   Treatment of Baboons with cH36-Fab (Fab fragment)

Three septic animals were treated with cH36-Fab look for any differences

5   between use of whole antibody and Fab fragment. Treatment protocols generally

followed procedures already discussed above. Although the group was too small for

detailed statistical analyses, the data suggested that the Fab fragment had effect in

attenuating sepsis-induced activation of coagulation, with increased TAT values and

depletion of fibrinogen similar to septic controls.   However, that effect was less

10   pronounced then results achieved with whole antibody. Correspondingly, there was

less consistent improvement in gas exchange (AaDO2), pulmonary hypertension

(PAM), and lung compliance (Cst) than in animals treated with whole cH36 antibody.

Biochemically, lung MPO values were similar to septic controls. Without wishing to

be bound to theory, the difference in effect between cH36 and its Fab fragment may

15   be due to the lower affinity of the Fab fragment for TF in the animal model.

EXAMPLE 9:   Anti-Tissue Factor Inhibition of Collagen-Induced Arthritis in

20   Transgenic Mice Expressing Human Tissue Factor

Collagen-induced arthritis (CIA) is an established experimental model of

rheumatoid arthritis which is induced in susceptible strains of mice following

immunization with type II collagen. In addition to the immune mediated mechanism

25   in the pathogenesis of rheumatoid arthritis, tissue factor initiated activation of the

coagulation cascade has also been implicated in the progression of the disease. Fibrin

deposition in the affected joints resulting from the activation of coagulation is

believed to contribute to synovial thickening and joint inflammation. To determine

whether treatment with anti-tissue factor antibodies will prevent development of

30   rheumatoid arthritis mice will be injected with cH36.

To induce CIA 7-12 week old mice are injected intradermally at the base of the tail with 100μg of type II collagen emulsified in Complete Freund's Adjuvant and given a boost injection with 100 μg of type II collagen emulsified in Incomplete Freund's Adjuvant at day 21. Immediately prior to the boost injection mice are given

5   0.3 mg anti-tissue factor antibody by IV injection (the control group are injected with PBS). Anti-tissue factor antibody injections (0.3 mg) are subsequently given weekly for the duration of the study (the control group are injected with PBS).

Animals are assessed for redness and swelling of the limbs and a clinical

10   score is allocated three times per week. The clinical severity is scored as follows: 1 point for each swollen digit except the thumb (maximum 4), 1 Point for the tarsal or carpal joint, and one point for the metatarsal or metacarpal joint with a maximum score of 6 for a hindpaw and 5 for a forepaw. Each paw is graded individually, the cumulative clinical arthritic score per mouse can reach a maximum of 22 points.

15

The present provisional application has information relating to published U.S. patent application no. 20030190705 which application is related to U.S Application No. 09/990,586 as filed on November 21, 2001, which application claims priority to U.S. Provisional Application USSN 60/343,306 as filed on October 29, 2001. The

20   U.S Application No. 09/990,586 is related to U.S. Application No. 09/293,854 (now U.S. Pat. No. 6,555,319) which application is a divisional of U.S. Application No. 08/814,806 (now U.S. Pat. No. 5,986,065) and the U.S. Application No. 10/230,880 claims priority to U.S Application No. 09/990,586. The disclosures of the U.S. Application Nos. 10/230,880, 09/990,586, 60/343,306 and U.S. Pat. Nos. 5,986,065

25   and 6,555,319 are each incorporated by reference. Also incorporated by reference is the disclosure of published U.S. patent application no. 20030190705.

The present provisional application is further related to U.S. provisional application Serial No. 60/480,254 as filed on June 19, 2003, the disclosure of which

30   is incorporated by reference.

The invention has been described in detail with reference to preferred embodiments thereof. However, it will be appreciated that those skilled in the art, upon consideration of the disclosure, may make modification and improvements within the spirit and scope of the invention. All references disclosed herein are incorporated herein by reference.

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What is claimed is:

1.   A method for preventing or treating a sepsis or inflammatory disease in a
mammal, the method comprising administering to the mammal a therapeutically
5   effective amount of at least one humanized antibody, chimeric antibody, or fragment
thereof that binds specifically to tissue factor (TF) to form a complex, wherein factor
X or factor IX binding to the complex is inhibited and the administration is sufficient
to prevent or treat the sepsis in the mammal.

10   2.   The method of claim 1, wherein the humanized antibody, chimeric antibody
or the fragment exhibits at least one of: 1) a dissociation constant (K_d) for the TF of
less than about 0.5 nM; or 2) an affinity constant (K_a) for the TF of less than about 10
x 10^{10} M^{-1}.

15   3.   The method of claims 1-2, wherein the humanized antibody, chimeric
antibody or fragment thereof is further characterized by having a binding specificity
for the TF about equal or greater than the antibody obtained from cell line H36.D2.B7
deposited under ATCC Accession No. HB-12255.

20   4.   The method of claims 1-3, wherein the humanized antibody, chimeric
antibody or fragment thereof is further characterized in that factor X or factor IX
activation by the TF-factor VIIa complex is blocked.

5.   The method of claims 1-4, wherein administration of the humanized antibody,
25   chimeric antibody or fragment to the mammal increases survival time by at least
about 2-fold as determined by a standard *in vivo* septic shock assay.

6.   The method of claims 1-5, wherein administration of the humanized antibody,
chimeric antibody or fragment to the mammal attenuates at least one of inflammatory
30   cytokine (interleukin-6 (IL-6) and interleukin-8 (IL-8), interleukin-1beta (IL-1β),

tumor necrosis factor-alpha (TNFα) or tumor necrosis factor receptor (TNFR)) levels
in the mammal after at least about 5 hours.

7.   The method of claims 1-6, wherein about 5 minutes after administration of the
humanized antibody, chimeric antibody or fragment, the mammal exhibits a blood
clotting time of between from about 30 to about 350 seconds as determined by a
standard prothrombin time assay.

8.   The method of claims 1-7, wherein the amount of the administered humanized
antibody, chimeric antibody, or fragment is sufficient to inhibit platelet deposition by
at least about 50% as determined by a standard platelet deposition assay.

9.   The method of claims 1-8, wherein the humanized antibody has an IgG1 or
IgG4 isotype.

10.   The method of claims 1-9, wherein the human TF binding fragment is Fab,
Fab', or F(ab)₂.

11.   The method of claims 1-10, wherein the humanized antibody is a monoclonal
antibody.

12.   The method of claims 1-10, wherein the humanized antibody or fragment
thereof is a single-chain.

13.   The method of claims 1-28, wherein the mammal is a primate.

14.   The method of claim 13, wherein the primate is a human patient.

15.   The method of claims 1-14, wherein the sepsis is associated with at least one
of disseminated intravascular coagulation (DIC), fibrin deposition, thrombosis, and
lung injury.

16.   The method of claims 1-14, wherein the inflammatory disease is associated with at least one of arthritis, preferably rheumatoid arthritis, glomerulonephritis, multiple sclerosis, psoriasis, Sjogren's syndrome and inflammatory bowel disease.

5

17.   The method of claims 1-28, wherein the amount of the humanized antibody, chimeric antibody or fragment administered to the mammal is between about 0.01 to about 25 (mg/kg).

10   18.   A kit for performing the method of claims 1-16, wherein the kit includes at least one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to human TF to form a complex, wherein factor X or factor IX binding to the complex is inhibited.

15   19.   The kit of claim 17, wherein the humanized antibody, chimeric antibody, or fragment thereof is provided in a pharmaceutically acceptable vehicle.

20.   The kit of claims 17-18, wherein the humanized antibody, chimeric antibody, or fragment thereof is lyophilized and the kit further includes a pharmaceutically

20   acceptable vehicle for dissolving the humanized antibody, chimeric antibody or fragment.

21.   A method for reducing an inflammatory cytokine production in a mammal, the method comprising administering to the mammal a therapeutically effective

25   amount of at least one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to TF to form a complex, wherein factor X or factor IX binding to the complex is inhibited and the administration is sufficient to reduce the inflammatory cytokine production in the mammal.

30   22.   The method of claim 21, wherein the inflammatory cytokine is at least one of inflammatory cytokine (interleukin-6 (IL-6) and interleukin-8 (IL-8), interleukin-

1beta (IL-1β), tumor necrosis factor-alpha (TNFα) or tumor necrosis factor receptor (TNFR)).

23.   The method of claims 21-22, wherein the administered antibody, chimeric

5   antibody or fragment there of is encompassed by any one of claims 2-12.

22.   A method for preventing or treating a sepsis-related condition in a mammal, the method comprising administering to the mammal a therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment thereof

10   that binds specifically to tissue factor (TF) to form a complex, wherein factor X or factor IX binding to the complex is inhibited and the administration is sufficient to prevent or treat the condition in the mammal.

23.   The method of claim 22, wherein the sepsis-related condition is one or more

15   of disseminated intravascular coagulation (DIC), fibrin deposition, thrombosis,lung injury, or sepsis-associated renal disorder .

24.   The method of claim 23, wherein the lung injury is acute lung injury (ALI), or acute respiratory distress syndrome (ARDS).

20

25.   The method of claim 23, wherein the sepsis-associated renal disorder is acute tubular necrosis (ACN).

26.   The method of claims 22-25, wherein the administered antibody, chimeric

25   antibody or fragment there of is encompassed by any one of claims 2-12.

27.   A method for preventing or treating sepsis-induced anemia in a mammal, the method comprising administering to the mammal a therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment thereof that binds

30   specifically to tissue factor (TF) to form a complex, wherein factor X or factor IX

binding to the complex is inhibited and the administration is sufficient to prevent or treat the condition in the mammal.

28.   The method of claim 27, wherein the administered antibody, chimeric

5   antibody or fragment there of is encompassed by any one of claims 2-12.

H36.D2.B7 Anti-Tissue Factor Light Chain Variable Domain

```
  GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTCTGGGAGAAAGTGTCACCATCACATGC
    D   I   Q   M   T   Q   S   P   A   S   Q   S   A   S   L   G   E   S   V   T   I   T   C

  CTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCAGGGAAATCTCCTCAGCTC
    L   A   S   Q   T   I   D   T   W   L   A   W   Y   Q   Q   K   P   G   K   S   P   Q   L

  CTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCAAGGTTCAGTGGCAGTGGATCTGGCACA
    L   I   Y   A   A   T   N   L   A   D   G   V   P   S   R   F   S   G   S   G   S   G   T

  AAATTTTCTTTCAAGATCAGCAGCCTACAGGCTGAAGATTTTGTAAATTATTACTGTCAACAAGTTTAC
    K   F   S   F   K   I   S   S   L   Q   A   E   D   F   V   N   Y   Y   C   Q   Q   V   Y

  AGTTCTCCATTCACGTTCGGTGCTGGGACCAAGCTGGAGCTGAAA
    S   S   P   F   T   F   G   A   G   T   K   L   E   L   K
```

FIG. 1A

FIG. 1B

H36.D3.B7 Anti-Tissue Factor Heavy Chain Variable Domain

GAGATCCAGCTGCAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGCAGGTATCCTGCAAG
E   I   Q   L   Q   Q   S   G   P   E   L   V   K   P   G   A   S   V   Q   V   S   C   K

ACTTCTGGTTACTCATTCACTGACTACAACGTGTACTGGGTGAGGCAGAGCCATGGAAAGAGCCTTGAG
T   S   G   Y   S   F   T   D   Y   N   V   Y   W   V   R   Q   S   H   G   K   S   L   E

20

TGGATTGGATATATTGATCCTTACAATGGTATTACTTACTATGATTACTATCTTCACAGAACTTCAAGGGCAAGGCCACA
W   I   G   Y   I   D   P   Y   N   G   I   T   I   Y   D   Q   N   F   K   G   K   A   T

TTGACTGTTGACAAGTCTTCCACCAGCCTTCATGCCATCTCAACAGCCTGACATCTGACGACTCTGCA
L   T   V   D   K   S   S   T   A   F   M   H   L   N   S   L   T   S   D   D   S   A

GTTTATTTCTGTGCAAGAGATGTGACTACGGCCCTTGACTTCTGGGGCCAAGGCACCACTCTCACAGTC
V   Y   F   C   A   R   D   V   T   T   A   L   D   F   W   G   Q   G   T   T   L   T   V

25

TCCTCA
S   S

CDR REGIONS UNDERLINED (single underline for nucleic acid sequence and double underline for amino acid sequence)

FIG. 2

Notes: 1. Amino acid sequence in one letter code.
        2. Immediately following the last residue of the framework 4(FR4)
            variable domain is the first residue of the constant domain for
            hOAT or hFAT.

```
FR1 (23 AA)              FR2 (15 AA)     FR3 (32 AA)                        FR4 (10 AA) Names
1        10       20     35              49 57 60       70       80         88 98      107
  DIQMTQSPASQSASLGESVTITC WYQQKPGKSPQLIY GVESRFSGSGSGTKFSFKISSLQAEDFVNYYC FGAGTKLELK cH36-LC
  DIQMTQSPASQSASLGESVTITC WYQQKPGKSPQLIY GVPSRFSGSGSGTKFSFKISSLQAEDFVNYYC FGAGTKLEIK LC-03
  DIQMTQSPASQSASLGESVTITC WYLQKPGKSPQLIY GVPS FSGSGSGTKFSFKISSLQAEDFVNYYC FGAGTKLEIK LC-04
  DIQMTQSPASLSASVGDRVTITC WYLQKPGKSPQLIY GVPSRFSGSGSGTKFSFKISSLQAEDFVNYYC FGQGTKLEIK LC-05
  DIQMTQSPASQSASLGESVTITC WYLQKPGKSPQLIY GVPSRFSGSGSGTKFSFKISSLQAEDFVNYYC FGQGTKLEIK LC-06
  DIQMTQSPASQSASLGESVTITC WYLQKPGKSPQLIY GVPSRFSGSGSGTDFSFTISSLQPEDFVNYYC FGQGTKLEIK LC-07
  DIQMTQSPASQSASLGESVTITC WYLQKPGKSPQLIY GVPSRFSGSGSGTDFSFTISSLQPEDFATYYC FGQGTKLEIK LC-08
  DIQMTQSPASLSASVGDRVTITC WYLQKPGKSPQLIY GVPSRFSGSGSGTDFSFTISSLQPEDFATYYC FGQGTKLEIK LC-09
  DIQMTQSPASLSASVGDRVTITC WYLQKPGKSPQLIY GVPSRFSGSGSGTDFSFTISSLQPEDFANYYC FGQGTKLEIK LC-10
  DIQMTQSPASLSASVGDRVTITC WYLQKPGKSPQLIY GVPSRFSGSGSGTKFSFTISSLQPEDFANYYC FGQGTKLEIK LC-11
  DIQMTQSPASLSASVGDRVTITC WYLQKPGQSPQLIY GVPSRFSGSGSGTKFSFTISSLQPEDFANYYC FGQGTKLEIK LC-12
```

FIG. 3A

Light Chain CDR Sequences of cH36

CDR1 (11 AA)
24   34
L A S Q T I D T W L A

FIG. 3B

CDR2 (7 AA)
50   56
A A T N L A D

FIG. 3C

CDR3 (9 AA)
89   97
Q Q V Y S S P F T

FIG. 3D

Exept for HC-08, all others HC mutants and cH36 contain F at position 64 in CDR2.
KC-08 has the mutation F64 to L (change from F to L at position 64)

```
     FR1 (30 AA)                    FR2 (14 AA)     FR3 (32 AA)                      FR4 (11 AA)   Names
     1        10        20    30 36                 49 67       75        85        95  107      117
  5  EIQLQQSGPELVKPGASVQVSCKTSGYSFT  WVRQSHGKSLEWIG  KATLTVDKSSTTAFMHLNSLTSDDSAVYFCAR  WGQGTTLTVSS  CH36-HC
     QIQLQQSGPELVKPGASVQVSCKTSGYSFT  WVRQSHGKSLEWIG  KATLTVDKSSTTAFMHLNSLTSDDSAVYFCAR  WGQGTTVTVSS  HC-01
     QIQLQQSGPELVKPGASVQVSCKTSGYSFT  WVRQSPGKGLEWIG  KATLTVDKSSTTAFMHLNSLTSDDSAVYFCAR  WGQGTTVTVSS  HC-02
     QIQLQQSGPELVKPGASVQVSCKTSGYSFT  WVRQSPGKGLEWIG  KATLTVDKSSTTAFMHLNSLRSEDTAVYFCAR  WGQGTTVTVSS  HC-03
     QIQLQQSGPELVKPGASVQVSCKTSGYSFT  WVRQSPGKGLEWIG  KATLTVDKSSTTAFMELSSLRSEDTAVYFCAR  WGQGTTVTVSS  HC-04
 10  QIQLQQSGPELVKPGASVQVSCKTSGYSFT  WVRQSPGKGLEWIG  KATLTVDKSSTAYMELSSLRSEDTAVYFCAR   WGQGTTVTVSS  HC-05
     QMQLQQSGGELVKPGASVRVSCKASGYSFT  WVRQSPGKGLEWIG  KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR  WGQGTTVTVSS  HC-06
     QIQLVQSGGELVKPGASVRVSCKASGYSFT  WVRQSPGKGLEWIG  KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR  WGQGTTVTVSS  HC-07
     QIQLVQSGGEVKKPGASVRVSCKASGYSFT  WVRQSPGKGLEWIG  KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR  WGQGTTVTVSS  HC-08
     QIQLVQSGGEVKKPGASVRVSCKASGYSFT  WVRQSPGKGLEWIG  KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR  WGQGTTVTVSS  HC-08R1
 15  QIQLVQSGPEVKKPGASVRVSCKASGYSFT  WVRQSPGKGLEWIG  KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR  WGQGTTVTVSS  HC-11
     QIQLVQSGPELKKPGASVRVSCKASGYSFT  WVRQSPGKGLEWIG  KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR  WGQGTTVTVSS  HC-12
     QIQLVQSGPEVKKPGASVRVSCKASGYSFT  WVRQSPGKGLEWIG  KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR  WGQGTTVTVSS  HC-09
     QIQLVQSGPEVVKPGASVRVSCKASGYSFT  WVRQSPGKGLEWIG  KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR  WGQGTTVTVSS  HC-10
```

FIG. 4A

Heavy Chain CDR Sequences

```
CDR1 (5aa)
31        35
D Y N V Y
D Y N V Y
```

FIG. 4B

```
     CDR2 (17 AA)
50                                66
Y I D P Y N G I T I Y D Q N F K G
Y I D P Y N G I T I Y D Q N L K G
```

FIG. 4C

```
     CDR3 (8AA)              Names
99              106
D V T T A L D F             cH36
D V T T A L D F             HC-08
```

FIG. 4D

Sequence of human kappa Light Chain Constant Domain:

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKH

KVYACEVTHQGLSSPVTKSFNRGEC

FIG. 5A

Sequence of human IgG1 Heavy Chain Constant Domain:

10 LEFASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC

NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV

HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL

15 VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIG. 5B

Notes: 1. Amino acid sequence in one letter code.
2. Immediatly following the last residue of the framework 4 (FR4)
    variable domain is the first residue of the constant domain for
    hOAT or hFAT.
3. LC constant are the same for hOAT and hFAT.

Sequence of human kappa Light Chain Constant Domain:

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEK

HKVYACEVTHQGLSSPVTKSFNRGEC

FIG. 6A

Sequence of human IgG4 Heavy Chain Constant Domain:

EFASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY

TCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGV

EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSL

TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

FIG. 6B

Notes: 1. Amino acid sequence in one letter code.
       2. Immediately following the last residue of the framework 4 (FR4)
          variable domain is the first residue of the constant domain for
          hOAT or hFAT.
       3. LC constant domain is the same for hOAT and hFAT.

FIG. 7A

FIG. 7B

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FIG. 7C

FIG. 7D

FIG. 8A

FIG. 8B

FIG. 8C

FIG. 9A

FIG. 9B

FIG. 10A

FIG. 10B

FIG. 10C

FIG. 10D

FIG. 11A

FIG. 11B

FIG. 12

FIG. 13A

FIG. 13B

SEQUENCE LISTING

            (1) GENERAL INFORMATION

5

        (i) APPLICANT:

           (ii) TITLE OF THE INVENTION:

10   (iii) NUMBER OF SEQUENCES: 26

        (iv) CORRESPONDENCE ADDRESS:
          (A) ADDRESSEE:
          (B) STREET:
15   (C) CITY:
          (D) STATE:
          (E) COUNTRY:
          (F) ZIP:

20   (v) COMPUTER READABLE FORM:
          (A) MEDIUM TYPE: Diskette
          (B) COMPUTER: IBM Compatible
          (C) OPERATING SYSTEM: DOS
          (D) SOFTWARE: FastSEQ Version 1.5
25

        (vi) CURRENT APPLICATION DATA:
          (A) APPLICATION NUMBER:
          (B) FILING DATE:
          (C) CLASSIFICATION:
30

       (vii) PRIOR APPLICATION DATA:
          (A) APPLICATION NUMBER:
          (B) FILING DATE:

35   (viii) ATTORNEY/AGENT INFORMATION:
          (A) NAME:
          (B) REGISTRATION NUMBER:
          (C) REFERENCE/DOCKET NUMBER:

40   (ix) TELECOMMUNICATION INFORMATION:
          (A) TELEPHONE:
          (B) TELEFAX:
          (C) TELEX:

45   (2) INFORMATION FOR SEQ ID NO:1:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 321 base pairs
          (B) TYPE: nucleic acid
50   (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: cDNA
       (iii) HYPOTHETICAL: NO
55   (iv) ANTISENSE: NO

```
            (v) FRAGMENT TYPE:
            (vi) ORIGINAL SOURCE:

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
5    GACATTCAGA TGACCCAGTC TCCTGCCTCC CAGTCTGCAT CTCTGGGAGA AAGTGTCACC
     60
     ATCACATGCC TGGCAAGTCA GACCATTGAT ACATGGTTAG CATGGTATCA GCAGAAACCA
     120
     GGGAAATCTC CTCAGCTCCT GATTTATGCT GCCACCAACT TGGCAGATGG GGTCCCATCA
10   180
     AGGTTCAGTG GCAGTGGATC TGGCACAAAA TTTTCTTTCA AGATCAGCAG CCTACAGGCT
     240
     GAAGATTTTG TAAATTATTA CTGTCAACAA GTTTACAGTT CTCCATTCAC GTTCGGTGCT
     300
15   GGGACCAAGC TGGAGCTGAA A
     321
            (2) INFORMATION FOR SEQ ID NO:2:


            (i) SEQUENCE CHARACTERISTICS:
20              (A) LENGTH: 107 amino acids
                (B) TYPE: amino acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear


25          (ii) MOLECULE TYPE: peptide
            (iii) HYPOTHETICAL: NO
            (iv) ANTISENSE: NO
            (v) FRAGMENT TYPE: N-terminal
            (vi) ORIGINAL SOURCE:
30
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:


     Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Gln Ser Ala Ser Leu Gly
     1               5                  10                  15
35   Glu Ser Val Thr Ile Thr Cys Leu Ala Ser Gln Thr Ile Asp Thr Trp
                 20                  25                  30
     Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Gln Leu Leu Ile
                 35                  40                  45
     Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
40      50                  55                  60
     Ser Gly Ser Gly Thr Lys Phe Ser Phe Lys Ile Ser Ser Leu Gln Ala
     65                  70                  75                  80
     Glu Asp Phe Val Asn Tyr Tyr Cys Gln Gln Val Tyr Ser Ser Pro Phe
                     85                  90                  95
45   Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
                    100                 105


            (2) INFORMATION FOR SEQ ID NO:3:

50          (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 351 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
55
            (ii) MOLECULE TYPE: DNA
```

```
             (iii) HYPOTHETICAL: NO
             (iv) ANTISENSE: NO
             (v) FRAGMENT TYPE:
             (vi) ORIGINAL SOURCE:
5
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

    GAGATCCAGC TGCAGCAGTC TGGACCTGAG CTGGTGAAGC CTGGGGCTTC AGTGCAGGTA
    60
10  TCCTGCAAGA CTTCTGGTTA CTCATTCACT GACTACAACG TGTACTGGGT GAGGCAGAGC
    120
    CATGGAAAGA GCCTTGAGTG GATTGGATAT ATTGATCCTT ACAATGGTAT TACTATCTAC
    180
    GACCAGAACT TCAAGGGCAA GGCCACATTG ACTGTTGACA AGTCTTCCAC CACAGCCTTC
15  240
    ATGCATCTCA ACAGCCTGAC ATCTGACGAC TCTGCAGTTT ATTTCTGTGC AAGAGATGTG
    300
    ACTACGGCCC TTGACTTCTG GGGCCAAGGC ACCACTCTCA CAGTCTCCTC A
    351
20
             (2) INFORMATION FOR SEQ ID NO:4:

             (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 117 amino acids
                 (B) TYPE: amino acid
25               (C) STRANDEDNESS: single
                 (D) TOPOLOGY: linear

             (ii) MOLECULE TYPE: peptide
30           (iii) HYPOTHETICAL: NO
             (iv) ANTISENSE: NO
             (v) FRAGMENT TYPE: N-terminal
             (vi) ORIGINAL SOURCE:

35           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

    Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
    1               5                   10                  15
    Ser Val Gln Val Ser Cys Lys Thr Xaa Gly Tyr Ser Phe Thr Asp Tyr
40              20                  25                  30
    Asn Val Tyr Trp Val Arg Gln Ser His Gly Lys Ser Leu Glu Trp Ile
            35                  40                  45
    Gly Tyr Ile Asp Pro Tyr Asn Gly Ile Thr Ile Tyr Asp Gln Asn Phe
            50                  55                  60
45  Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Phe
    65                  70                  75                  80
    Met His Leu Asn Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys
                    85                  90                  95
    Ala Arg Asp Val Thr Thr Ala Leu Asp Phe Trp Gly Gln Gly Thr Thr
50              100                 105                 110
    Leu Thr Val Ser Ser
                115

             (2) INFORMATION FOR SEQ ID NO:5:
55
             (i) SEQUENCE CHARACTERISTICS:
```

           (A) LENGTH: 7 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

5

           (ii) MOLECULE TYPE: peptide
           (iii) HYPOTHETICAL: NO
           (iv) ANTISENSE: NO
           (v) FRAGMENT TYPE: N-terminal
10   (vi) ORIGINAL SOURCE:

           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

    Leu Ala Ser Gln Thr Ile Asp
15 1   5

           (2) INFORMATION FOR SEQ ID NO:6:

           (i) SEQUENCE CHARACTERISTICS:
20   (A) LENGTH: 7 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

25   (ii) MOLECULE TYPE: peptide
           (iii) HYPOTHETICAL: NO
           (iv) ANTISENSE: NO
           (v) FRAGMENT TYPE: N-terminal
           (vi) ORIGINAL SOURCE:
30   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

    Ala Ala Thr Asn Leu Ala Asp
    1   5

35   (2) INFORMATION FOR SEQ ID NO:7:

           (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 9 amino acids
           (B) TYPE: amino acid
40   (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

           (ii) MOLECULE TYPE: peptide
           (iii) HYPOTHETICAL: NO
45   (iv) ANTISENSE: NO
           (v) FRAGMENT TYPE: N-terminal
           (vi) ORIGINAL SOURCE:

           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
50
    Gln Gln Val Tyr Ser Ser Pro Phe Thr
    1   5

           (2) INFORMATION FOR SEQ ID NO:8:
55
           (i) SEQUENCE CHARACTERISTICS:

```
            (A) LENGTH: 6 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
 5
        (ii) MOLECULE TYPE: peptide
        (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
        (v) FRAGMENT TYPE: N-terminal
10      (vi) ORIGINAL SOURCE:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

    Thr Asp Tyr Asn Val Tyr
15   1               5

            (2) INFORMATION FOR SEQ ID NO:9:

        (i) SEQUENCE CHARACTERISTICS:
20          (A) LENGTH: 17 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

25      (ii) MOLECULE TYPE: peptide
        (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
        (v) FRAGMENT TYPE: N-terminal
        (vi) ORIGINAL SOURCE:
30
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

    Tyr Ile Asp Pro Tyr Asn Gly Ile Thr Ile Tyr Asp Gln Asn Phe Lys
     1               5                   10                  15
35  Gly

            (2) INFORMATION FOR SEQ ID NO:10:

        (i) SEQUENCE CHARACTERISTICS:
40          (A) LENGTH: 8 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

45      (ii) MOLECULE TYPE: peptide
        (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
        (v) FRAGMENT TYPE: N-terminal
        (vi) ORIGINAL SOURCE:
50
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

    Asp Val Thr Thr Ala Leu Asp Phe
     1               5
55
            (2) INFORMATION FOR SEQ ID NO:11:
```

```
                    (i) SEQUENCE CHARACTERISTICS:
                      (A) LENGTH: 21 base pairs
                      (B) TYPE: nucleic acid
     5                (C) STRANDEDNESS: single
                      (D) TOPOLOGY: linear

                    (ii) MOLECULE TYPE: DNA
                    (iii) HYPOTHETICAL: NO
    10              (iv) ANTISENSE: NO
                    (v) FRAGMENT TYPE:
                    (vi) ORIGINAL SOURCE:

                    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
    15
        CTGGCAAGTC AGACCATTGA T
           21

                        (2) INFORMATION FOR SEQ ID NO:12:
    20
                    (i) SEQUENCE CHARACTERISTICS:
                      (A) LENGTH: 21 base pairs
                      (B) TYPE: nucleic acid
                      (C) STRANDEDNESS: single
    25                (D) TOPOLOGY: linear

                    (ii) MOLECULE TYPE: DNA
                    (iii) HYPOTHETICAL: NO
                    (iv) ANTISENSE: NO
    30              (v) FRAGMENT TYPE:
                    (vi) ORIGINAL SOURCE:

                    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

    35  GCTGCCACCA ACTTGGCAGA T
           21

                        (2) INFORMATION FOR SEQ ID NO:13:

    40              (i) SEQUENCE CHARACTERISTICS:
                      (A) LENGTH: 28 base pairs
                      (B) TYPE: nucleic acid
                      (C) STRANDEDNESS: single
                      (D) TOPOLOGY: linear
    45
                    (ii) MOLECULE TYPE: DNA
                    (iii) HYPOTHETICAL: NO
                    (iv) ANTISENSE: NO
                    (v) FRAGMENT TYPE:
    50              (vi) ORIGINAL SOURCE:

                    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

        CAACAAGTTT ACAGTTCTCC ATTCACGT
    55     28
```

        (2) INFORMATION FOR SEQ ID NO:14:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 18 base pairs
 5   (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA
10   (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
        (v) FRAGMENT TYPE:
        (vi) ORIGINAL SOURCE:

15   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

    ACTGACTACA ACGTGTAC
    18
              (2) INFORMATION FOR SEQ ID NO:15:
20
        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 51 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
25   (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA
        (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
30   (v) FRAGMENT TYPE:
        (vi) ORIGINAL SOURCE:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

35   TATATTGATC CTTACAATGG TATTACTATC TACGACCAGA ACTTCAAGGG C
     51
              (2) INFORMATION FOR SEQ ID NO:16:

40   (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 24 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
45
        (ii) MOLECULE TYPE: cDNA
        (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
        (v) FRAGMENT TYPE:
50   (vi) ORIGINAL SOURCE:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

    GATGTGACTA CGGCCCTTGA CTTC
55   24
              (2) INFORMATION FOR SEQ ID NO:17:

5

```
        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 23 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA
        (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
        (v) FRAGMENT TYPE:
        (vi) ORIGINAL SOURCE:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

    GCACCTCCAG ATGTTAACTG CTC
        23


            (2) INFORMATION FOR SEQ ID NO:18:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 20 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA
        (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
        (v) FRAGMENT TYPE:
        (vi) ORIGINAL SOURCE:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
    GAARTAVCCC TTGACCAGGC
    20


            (2) INFORMATION FOR SEQ ID NO:19:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 35 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA
        (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
        (v) FRAGMENT TYPE:
        (vi) ORIGINAL SOURCE:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

    GGAGGCGGCG GTTCTGACAT TGTGMTGWCM CARTC
        35


            (2) INFORMATION FOR SEQ ID NO:20:
```

            (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 45 base pairs
               (B) TYPE: nucleic acid
5   (C) STRANDEDNESS: single
               (D) TOPOLOGY: linear

            (ii) MOLECULE TYPE: DNA
            (iii) HYPOTHETICAL: NO
10   (iv) ANTISENSE: NO
            (v) FRAGMENT TYPE:
            (vi) ORIGINAL SOURCE:

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
15
    ATTTCAGGCC CAGCCGGCCA TGGCCGARGT YCARCTKCAR CARYC
      45

                (2) INFORMATION FOR SEQ ID NO:21:
20
            (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 33 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: single
25   (D) TOPOLOGY: linear

            (ii) MOLECULE TYPE: DNA
            (iii) HYPOTHETICAL: NO
            (iv) ANTISENSE: NO
30   (v) FRAGMENT TYPE:
            (vi) ORIGINAL SOURCE:

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

35   CCCGGGCCAC CATGKCCCCW RCTCAGYTYC TKG
      33

                (2) INFORMATION FOR SEQ ID NO:22:

40   (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 35 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: single
               (D) TOPOLOGY: linear
45
            (ii) MOLECULE TYPE: DNA
            (iii) HYPOTHETICAL: NO
            (iv) ANTISENSE: NO
            (v) FRAGMENT TYPE:
50   (vi) ORIGINAL SOURCE:

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

    CCCGGGCCAC CATGGRATGS AGCTGKGTMA TSCTC
55   35

                     (2) INFORMATION FOR SEQ ID NO:23:

                 (i) SEQUENCE CHARACTERISTICS:
                     (A) LENGTH: 52 base pairs
    5   (B) TYPE: nucleic acid
                     (C) STRANDEDNESS: single
                     (D) TOPOLOGY: linear

                 (ii) MOLECULE TYPE: DNA
   10   (iii) HYPOTHETICAL: NO
                 (iv) ANTISENSE: NO
                 (v) FRAGMENT TYPE:
                 (vi) ORIGINAL SOURCE:

   15   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

        ATATACTCGC GACAGCTACA GGTGTCCACT CCGAGATCCA GCTGCAGCAG TC
        52

   20   (2) INFORMATION FOR SEQ ID NO:24:

                 (i) SEQUENCE CHARACTERISTICS:
                     (A) LENGTH: 31 base pairs
                     (B) TYPE: nucleic acid
   25   (C) STRANDEDNESS: single
                     (D) TOPOLOGY: linear

                 (ii) MOLECULE TYPE: DNA
                 (iii) HYPOTHETICAL: NO
   30   (iv) ANTISENSE: NO
                 (v) FRAGMENT TYPE:
                 (vi) ORIGINAL SOURCE:

                 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
   35
        GACCTGAATT CTAAGGAGAC TGTGAGAGTG G
        31

                   (2) INFORMATION FOR SEQ ID NO:25:
   40
                 (i) SEQUENCE CHARACTERISTICS:
                     (A) LENGTH: 29 base pairs
                     (B) TYPE: nucleic acid
                     (C) STRANDEDNESS: single
   45   (D) TOPOLOGY: linear

                 (ii) MOLECULE TYPE: DNA
                 (iii) HYPOTHETICAL: NO
                 (iv) ANTISENSE: NO
   50   (v) FRAGMENT TYPE:
                 (vi) ORIGINAL SOURCE:

                 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

   55   TTAATTGATA TCCAGATGAC CCAGTCTCC
        29

        (2) INFORMATION FOR SEQ ID NO:26:

        (i) SEQUENCE CHARACTERISTICS:
 5   (A) LENGTH: 45 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

10   (ii) MOLECULE TYPE: DNA
        (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
        (v) FRAGMENT TYPE:
        (vi) ORIGINAL SOURCE:
15
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

    TAATCGTTCG AAAAGTGTAC TTACGTTTCA GCTCCAGCTT GGTCC
    45
20

A.   CLASSIFICATION OF SUBJECT MATTER

IPC(7)   :   A61K 39/40, 39/42, 39/395; G01N 33/53; C12P 21/08; C07K 16/00

US CL   :   424/133.1, 134.1, 141.1, 146.1; 435/7.1; 530/387.3, 388.1, 388.26

According to International Patent Classification (IPC) or to both national classification and IPC

B.   FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 424/133.1, 134.1, 141.1, 146.1; 435/7.1; 530/387.3, 388.1, 388.26

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Continuation Sheet

C.   DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 03/029295 A1, 10 April 2003 (see entire document)	1-2, 4-17, 21-28 ----------- 3, 18-20,
Y	US 5,986,065 (Wong et al.) 16 November 1999 (see entire document)	1-28
Y	US 5,223,427 (Edgington et al.) 29 June 1993 (see entire document)	1-28
X/E	US 6,703,494 (Kirchhofer et al.) 9 March 2004 (see entire document)	1-28

☐ Further documents are listed in the continuation of Box C.   ☐ See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance		
"E"	earlier application or patent published on or after the international filing date	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
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"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed	"&"	document member of the same patent family

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Continuation of B. FIELDS SEARCHED Item 3:
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ance Notes on Codes and Abbreviations" appearing at the begin-
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(54) Title: COMPOSITIONS AND METHODS FOR TREATING COAGULATION RELATED DISORDERS

(57) Abstract: Disclosed are methods for preventing or treating sepsis, a sepsis-related condition or an inflammatory disease in
a mammal. In one embodiment, the method includes administering to the mammal a therapeutically effective amount of at least
one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to tissue factor (TF) to form a complex in
which factor X or factor IX binding to the complex is inhibited and the administration is sufficient to prevent or treat the sepsis in
the mammal. The invention has a wide spectrum of useful applications including treating sepsis, disorders related to sepsis, and
inflammatory diseases such as arthritis.

5

COMPOSITIONS AND METHODS FOR TREATING
COAGULATION RELATED DISORDERS

10 **FIELD OF THE INVENTION**

The present invention features compositions and methods for preventing or
treating disorders that relate to undesired activation of blood coagulation. In some
instances, the coagulation contributes to certain inflammatory diseases and related
disorders. In one aspect, the invention provides methods for treating such disorders

15 by administering a therapeutically effective amount of a chimeric or humanized
antibody that binds tissue factor (TF) specifically. The invention has a wide spectrum
of important applications including use in the prevention or treatment of
inflammation including sepsis and arthritis.

20 **BACKGROUND OF THE INVENTION**

There is increasing recognition of relationship between coagulation and
inflammation. For instance, certain coagulation factors are thought to activate pro-
inflammatory cells and elicit inflammatory responses. On the other hand, some pro-
inflammatory cytokines have been reported to induce TF expression and generate

25 coagulation factors. Studies in certain primates support existence of the relationship
by showing that certain anticoagulants reduce inflammation. See F. B. Taylor Jr. *et
al., J. Clin. Invest.* **79**:918-925 (1987); M. Levi *et al., J. Clin. Invest.* **93**:114-120
(1994); and M. C. Minnema *et al., Blood* **95**:1117-23 (2000).

30   Much has been reported about blood coagulation. For instance, thrombin is a
blood protein that is believed to provide a link between coagulation and
inflammation. Most thrombin is generated by TF-initiation of the coagulation
cascade. Other key coagulation factors include Factor VIIa and Factor Xa.

Thrombin is thought to occupy multiple roles in pro-coagulant, anticoagulant, inflammatory, and mitogenic responses. See generally L. Styer, *Biochemistry*, 3rd Ed., W.H. Freeman Co., New York; and A.G. Gilman *et al.*, in *The Pharmacological Basis of Therapeutics*, 8th Ed., McGraw-Hill Inc., New York.

5

Certain infectious agents are thought to disturb the TF-initiated coagulation cascade. Fortunately, localized activation of the coagulation cascade often keeps the disturbance in check. Sometimes however, aberrant TF expression leads to serious and potentially life-threatening thrombotic disorders. For example, it has been

10   suggested that bacterial induction of TF expression can lead to sepsis, disseminated intravascular coagulation (DIC), widespread fibrin deposition, and other complications. The increase in TF expression is thought to be an important factor in facilitating progression of these disorders. An example of progression of an inflammatory disorder is the progression of acute lung injury (ALI) to acute

15   respiratory distress syndrome (ARDS) followed by progressive injury involving additional organ systems, such as the kidneys, leading to progressively more severe forms of sepsis. See Welty-Wolf, K. *et al. Am. J. Respir. Crit. Care Med.* **164**:1988 (2001), for instance.

20   There have been attempts to understand coagulation related disorders such as sepsis.

For instance, sepsis is a term that has used to characterize a spectrum of clinical conditions facilitated by a host immune response to infection, trauma, or

25   both. Sepsis has been characterized as an uncontrolled cascade of blood coagulation, fibrinolysis, and inflammation. At certain steps in the cascade, an auto-amplification process contributes to an acceleration of coagulation abnormalities, undesired inflammation, and endothelial injury. The amplification process is the result of inflammatory cytokines up-regulating the expression of TF on cells such as

30   endothelial cells and monocytes, resulting in increased activation of the coagulation cascade, which in turn results in the activation of PAR receptors and the up-

regulation of the production of inflammatory cytokines. See Osterud, B. *et al.*, *Thromobsis Hemost.* **83**:861 (2000); Mechtcheriakova, D. *et al.*, *FASEB J.* **15**:230 (2001); Shen, B.-Q. *et al.*, *J. Biol. Chem.* **276**:5281 (2001).

5   More specifically, sepsis has been characterized by systemic activation of inflammation and blood coagulation. Fibrinolyisis can be suppressed. Some research has pointed to a hemostatic imbalance that is thought to promote e.g., DIC and microvascular thrombosis. These and related indication are believed to impact normal organ function which can lead to death.

10

Sepsis and related disorders continue to be linked to patient contact with hospitals and out-patient clinics. Accordingly, managing these disorders is a prime concern of many health administrators, clinicians and insurers.

15   There are reports that undesired activation of blood coagulation is a key feature of certain inflammatory diseases. For example, extravascular fibrin deposition has been found in the autoimmune lesions of patients with rheumatoid arthritis (RA), glomerulonephritis, multiple sclerosis, psoriasis, Sjogren's syndrome and inflammatory bowel disease. See Weinberg, *et al.*, *Arthritis Rheum.* **34**:996-1005

20   (1991); Wakefield, *et al.*, *J Clin Pathol* **47**:129-133 (1994); Schoph, *et al.*, *Arch Dermatol Res* **285**:305-309 (1993); Zeher, *et al.*, *Clin Immunol Immunopathol* **71**:149-155 (1994); More, *et al.*, *J Clin Pathol* **46**:703-708 (1993).

Moreover, elevated TF levels are thought to be associated with systemic lupus

25   erythematosus. See Segal, *et al.*, *J Rheumatol* **27**:2827-2832 (2000). See also Nakano, *et al.*, *Clin Exp Rheumatol* **17**:161-170 (1999); Morris, *et al.*, *Ann Rheum Dis* **53**:72-79 (1994); Furmaniak-Kazmierczak, *et al.*, *J Clin Invest* **94**:472-480 (1994); Bokarewa, *et al.*, *Inflamm Res* **51**:471-477 (2002).

30   There have been suggestions that certain inflammatory conditions may be treated by blocking thrombosis. See R. Gordon *et al.*, *The New England Journal of*

Medicine **344**:699-709, 759-762 (2001). Certain anti-TF antibodies have been reported to be of some help in reducing some types of inflammation. See Levi, M. *et al., supra.*

5   There have been efforts to develop antibodies that bind blood coagulation factors.

           For instance, U.S. Pat. Nos. 5,986,065 and 6,555,319 to Wong, H. *et al.* and PCT/US98/04644 (WO 98/40408) disclose a variety of such antibodies. Specifically

10   provided are murine antibodies, chimeric antibody derivatives and fragments thereof with significant binding affinity and specificity for tissue factor (TF). Use of chimeric antigen binding molecules are believed to reduce risk of an undesired immune response in human patients. See also S. L.Morrison and V. Oi, *Adv. Immunol.* **44**:65 (1989) (reporting methods of making human-mouse chimeric

15   antibodies).

           A variety of approaches have been used to make antibodies more immunologically acceptable to humans. Some use recombinant DNA technologies. For instance, one strategy has been to clone and modify non-human antibodies to

20   more closely resemble human antibodies. Collectively, such antibodies have been referred to as "humanized". See U.S Pat. Nos. 5,766,886 to Studnicka *et al.*; 5,693,762 to Queen *et al.*; 5,985,279 to Waldeman *et al.*; 5,225,539 to Winter; 5,639,641 to Pedersen, *et al.*; and references cited therein for methods of making and using humanized antibodies.

25

           Additional strategies for making humanized antibodies have been reported. See E. Padlan *Mol. Immunol.* **28**:489 (1991); Jones *et al., Nature* **321**:522-525 (1986); Junghans *et al., supra*; and Roguska, *et al., PNAS (USA)* **91**:969 (1994). See also published U.S Patent Applications 2003/0109860 A1 and 2003/0082636.

30

It is unclear if prior antibodies are robust enough to block or reduce undesired activation of blood coagulation. More specifically, it is unclear if such antibodies are potent enough to prevent or treat sepsis and inflammatory diseases such as arthritis.

5 **SUMMARY OF THE INVENTION**

The present invention features compositions and methods for preventing or treating disorders relating to undesired activation of blood coagulation. In one aspect, the invention provides methods for preventing or treating such disorders by administering to a mammal a therapeutically effective amount of a chimeric or

10 humanized antibody that binds tissue factor (TF). The invention has a wide spectrum of important applications including use in the treatment of sepsis and inflammatory diseases such as arthritis.

We have found that antibodies and antigen binding fragments thereof that

15 specifically bind an epitope predominant to native human TF are suitable for preventing or treating disorders relating to undesired activation of blood coagulation. Preferred antibodies and fragments specifically bind native human TF and do not substantially bind non-native or denatured TF. More particular antibodies and fragments suitable for use with the present invention bind human TF so that at least

20 one of Factor X (FX) and Factor IX (FIX) do not effectively bind to the TF-Factor VIIa complex. Additionally preferred antibodies and fragments reduce or block TF function, typically by reducing or blocking FX binding or gaining access to TF molecules. Further preferred antibodies and fragments suitable for use with the invention do not significantly inhibit or block interaction or binding between TF and

25 Factor VIIa, or inhibit or block activity of a TF-Factor VIIa complex with respect to materials other than FX or FIX.

As discussed, it is believed that undesired activation of blood coagulation underlies sepsis and a variety of specific inflammatory diseases. More specifically,

30 unwanted TF-mediated coagulation is thought to initiate and/or prolong such disorders in many cases. It is thus an object of the present invention to provide

antibodies and fragments thereof that specifically bind TF to reduce or inactivate many if not all TF-associated functions. Such functions include, but are not limited to, blocking or inhibiting at least one of FIX and FX binding to the TF complex. Without wishing to be bound to theory, it is believed that by blocking or inhibiting

5   binding of at least one of those factors to the TF complex, activation of unwanted blood coagulation can be reduced or in some cases eliminated. That is, by blocking or inhibiting such unwanted processes according to the invention, it is believed that it is possible to prevent, treat or alleviate symptoms associated with sepsis and specific inflammatory diseases.

10

Preferably, such antibodies and fragments thereof are chimeric or humanized and are generally suitable for use in primates and particularly human patients in need of treatment.

15   There is recognition that sepsis and related conditions result from a potent and potentially life-threatening immune response to infection, trauma, or both. Typically, blood throughout the vasculature is subject to coagulation, resulting in complications such as inflammation, disseminated intravascular coagulation (DIC), clotting, and organ distress. Death can ensue in a matter of hours or less unless the condition is

20   treated rapidly. Prior to the present invention, it was not clear if any anti-TF antibody or TF-binding fragment would be robust enough to prevent or treat sepsis and related conditions.

However, it has been found that the anti-TF binding antibodies described

25   herein are robust enough (*i.e.*, bind human TF specifically enough and with appropriate avidity) to inhibit or block unwanted activation of the coagulation cascade. It has also been found that such activity is beneficial and can be used to prevent or treat sepsis and related conditions. As discussed below, we have found that such antibodies and fragments show good attenuation of inflammation,

30   disseminated intravascular coagulation (DIC), clotting, organ distress and related conditions in an *in vivo* animal model of human sepsis.

Such potent blocking or inhibition of the blood coagulation cascade has also been found to be highly useful in the prevention or treatment of certain inflammatory diseases. Without wishing to be bound to theory, it is believed that by using the

5   invention to block or reduce undesired activation of blood coagulation, it is possible to prevent, treat or alleviate symptoms associated with one or a combination of the inflammatory diseases. Importantly, the anti-TF binding antibodies described herein have been found to be robust enough to inhibit or block unwanted activation of the coagulation cascade, thereby helping to prevent, treat or alleviate symptoms

10   associated with arthritis and other inflammatory diseases.

Accordingly, and in one aspect, the invention provides a method for preventing or treating at least one of sepsis and an inflammatory disease in a mammal. In one embodiment, the method includes administering to the mammal a

15   therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to human TF to form a complex. A more preferred antibody reduces or blocks at least one of FX and FIX binding to the complex. Practice of the method is highly useful for preventing, treating, or reducing the severity of symptoms associated with sepsis and inflammatory diseases

20   including, but not limited to, rheumatoid arthritis (RA).

The present invention provides other important uses and advantages.

For instance, we have discovered that preferred humanized antibodies,

25   chimeric antibodies and fragments thereof desirably block at least one of FX and FIX binding to the TF-FVIIa complex. Preferably, such antibodies and fragments also inhibit or block FX or FIX activation by the complex. Surprisingly, such antibodies, when tested in the *in vivo* animal of human sepsis provided herein, are robust enough to prevent, treat or alleviate symptoms of sepsis and related complications. Also

30   surprisingly, such preferred antibodies and fragments are robust enough to prevent, treat, or alleviate symptoms associated with particular inflammatory diseases.

7

Importantly, preferred use of the present invention has identified and takes advantage of a particular immunological target (epitope) on the human TF molecule that can be exploited to prevent, treat, or alleviate symptoms associated with these indications.

5   The invention is flexible and can be used in a variety of settings in which sepsis and inflammatory diseases may be suspected or predominate.

        For instance, and in one embodiment, the invention can be used in hospitals, clinics and other medical settings where sepsis has become a major health problem.
10   Especially problematic has been emergence of antibiotic resistance microorganisms such as bacteria which, if present in the blood, can rapidly produce septic shock and related complications. Practice of the invention can be used to hold the sepsis or related condition at bay while caregivers identify an appropriate treatment protocol, or perhaps reverse the effects of sepsis. It is thus anticipated as an object of the
15   invention to provide sepsis prevention or treatment methods in which administration of the antibodies and fragments disclosed herein may be combined with administration of one or more antibiotics.

        The invention finds further use in emergency medical settings (e.g.,
20   ambulance, combat) in which the prevention and treatment methods disclosed herein can be administered at the point of care. Thus in one invention embodiment, the sepsis or sepsis-related condition can be held under some control while the patient is transported to a hospital or clinic for evaluation and treatment.

25   In other invention embodiments, the invention can be used to prevent, treat or reduce symptoms associated with arthritis and especially rheumatoid arthritis. For instance, by blocking or reducing the unwanted activation of blood coagulation, it is now possible to reduce the painful inflammation, pathological tissue destruction and remodeling typically associated with arthritis and related inflammatory diseases.
30

In another aspect, the invention provides a kit for performing the methods of this invention. In one embodiment, the kit includes at least one humanized antibody, chimeric antibody, or fragment thereof provided herein.

5   The invention also provides a method for reducing cytokine production in a mammal. In one embodiment, the method includes administering to the mammal a therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to tissue factor (TF) to form a complex. Preferably, Factor X or Factor IX binding to the complex is inhibited and 10   the administration is sufficient to reduce the cytokine production in the mammal. Suitable humanized antibodies, chimeric antibodies and fragments thereof are disclosed above and in the discussion and examples that follow.

      Further provided by the present invention is a method for preventing or 15   treating a sepsis-related condition in a mammal. In one embodiment, the method includes administering to the mammal a therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to tissue factor (TF) to form a complex. Preferred antibodies and fragments are described herein and include those in which Factor X or factor IX 20   binding to the complex is inhibited. Preferably, administration is sufficient to prevent or treat the condition in the mammal.

      The invention further provides a method for preventing or treating sepsis-induced anemia in a mammal. In one embodiment, the method includes 25   administering to the mammal a therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to tissue factor (TF) to form a complex. Preferred antibodies and fragments are disclosed herein including those in which Factor X or Factor IX binding to the complex is inhibited. Preferably, the administration is sufficient to prevent or treat 30   the condition in the mammal.

Other aspects of the invention are discussed *infra*.

BRIEF DESCRIPTION OF THE DRAWINGS

Figs. 1A and 1B shows the nucleic acid (SEQ ID NOS: 1 and 3) and amino

5   acid (SEQ ID NOS: 2 and 4) sequences of light chain and heavy chain variable

domains of H36.D2.B7, the murine anti-tissue factor antibody, with hypervariable

regions (CDRs or Complementarity Determining Regions) underlined (single

underline for nucleic acid sequences and double underline for amino acid sequences).

10   Fig. 2 is a drawing showing a plasmid map of humanized anti-TF IgG1

antibody expression vector (pSUN-34).

Figs. 3A-D are sequences of partially and fully humanized light chain (LC)

variable domains of the anti-TF antibody (SEQ ID NO.: ____). Fig. 3A shows the

15   sequence named "LC-09" which is representative of a fully humanized LC

framework (SEQ ID NO.:____). Light chain CDR sequences of cH36 and LC-09 are

shown in Figs. 3B-D (SEQ ID NOS.: _____, respectively).

Figs. 4A-D are drawings showing the sequences of partially and fully

20   humanized heavy chain (HC) variable domains of the anti-TF antibody (SEQ ID

NOS.: _____). Fig. 4A shows the sequence named "HC-08" which is representative

of a fully humanized HC framework (SEQ ID NO.:____). Heavy chain CDR

sequences for cH36 and HC-08 are shown in Figs. 4B-D (SEQ ID NOS.: _____,

respectively).

25

Figs. 5A-B are sequences showing human constant domains in the IgG1 anti-

tissue factor antibody (hOAT), with Fig. 5A showing the human kappa light chain

constant domain (SEQ ID NO.: ____·) and Fig. 5B showing the human IgG1 heavy

chain constant domain (SEQ ID NO.: ___). The figures show hOAT (IgG1) constant

30   domain amino acid sequences.

10

Figs. 6A-B are sequences showing human constant domains in the IgG4 anti-tissue factor antibody (hFAT) with Fig. 6A showing the human kappa light chain constant domain (SEQ ID NO.: ____) and Fig. 6B showing the human IgG4 heavy chain constant domain (SEQ ID NO.: _____).

5

Figs. 7A-D are graphs showing a change in plasma IL-6 and IL-8 (Figs. 7A-B) concentrations (Figs. 7A-B); or IL-1β and TNF-α concentrations (Figs. 7C-D) in rhesus monkeys following an infusion of live *E.coli* in a lethal sepsis model.

10   Figs. 8A-C are graphs showing that cH36 attentuates sepsis-induced acute lung injury (ALI). In the figures, AaDO$_2$ is in mmHg, time in hours, pulmonary system compliance (Cst) in ml/cm water, and pulmonary arterial pressure (PAM) in mmHg.

15   Figures. 9A-B are graphs showing Kidney Myeloperoxidase (A) and Small Bowel Wet/Dry Weight Ratio (B) in Baboons.

Figure 10A-D are graphs showing that cH36 attenuates sepsis and related conditions in baboons. cH36 attenuates sepsis-induced coagulopathy (fibrinogen in
20   mg/DL; time in hours; partial prothrombin time (PTT) in seconds; and TAT in micrograms/L).

Figures 11A-B are graphs showing that elevations in serum IL-8 (A) and IL-6(B) are attenuated by treatment with cH36.

25

Figure 12 is a graph showing that elevations in bronchial alveolar levage IL-8, IL-6 and TNFR1 levels attenuated by treatment with cH36.

Figures 13A-C are graphs showing mean urine output (13A), mean blood pH
.30   (13B), and serum bicarbonate levels (13C) in baboons treated with control and cH36 antibodies.

DETAILED DESCRIPTION OF THE INVENTION

As discussed, the invention provides a method for preventing, treating, or alleviating symptoms associated with sepsis or inflammatory diseases such as

5   arthritis. Practice of the method involves administering to a mammal in need of such treatment a therapeutically effective amount of at least one of a humanized antibody, chimeric antibody, or human TF-binding fragment to prevent or treat these diseases and related conditions.

10   There have been efforts to understand the etiology of sepsis and conditions related to sepsis. For instance, there is recognition that early events in the sepsis cascade are triggered by the host's immune response, thereby facilitating damaging actions on the vascular endothelium. Subendothelial structures are exposed and collagenases are liberated. Endothelial cells expressing tissue factor (TF) are

15   exposed, triggering the extrinsic pathway for activation of the coagulation cascade and accelerating the production of thrombin. Concurrently, the endothelial damage causes further exacerbation of inflammation, resulting in neutrophil activation, neutrophil-endothelial cell adhesion, and further elaboration of inflammatory cytokines. These inflammatory processes further contribute to vascular endothelial

20   dysfunction. Endogenous modulators of homeostasis, such as protein C and anti-thrombin III (AT III), are consumed and their levels become deficient as the body attempts to return to a normal functional state. Under normal conditions, the endothelial surface proteins thrombomodulin and endothelial protein C receptor (EPCR), activate protein C and its modulating effects. In sepsis, the endothelial

25   damage impairs this function of thrombomodulin and EPCR, thereby contributing to the loss of control. Left unopposed, the endothelial damage accumulates. This uncontrolled cascade of inflammation and coagulation fuels the progression of sepsis, resulting in hypoxia, widespread ischemia, organ dysfunction, and ultimately death for a large number of patients.

30

By the phrase "sepsis-related condition" is meant those known to precede, accompany, or follow sepsis including, but not limited to, disseminated intravascular coagulation (DIC), fibrin deposition, thrombosis, and lung injury, including acute lung injury (ALI), or acute respiratory distress syndrome (ARDS). A particular type

5   of lung injury amenable to prevention or treatment by use of the invention is sepsis-induced acute lung injury. See Welty-Wolf, *et al., Am. J. Respir. Crit. Care Med.* **164**:1988 (2001), for instance. Also encompassed are certain renal disorders accompanying sepsis such as acute tubular necrosis (ACN) and related conditions.

10   Acute lung injury (ALI) and acute respiratory distress syndrome (ARDS) are severe disorders that continue to receive significant attention. In particular, an important feature of ALI and ARDS, is local activation of extrinsic coagulation and inhibition of fibrinolysis. As the injury evolves, these perturbations have been reported to cause deposition of fibrin in the microvascular, interstitial, and alveolar

15   spaces of the lung leading to capillary obliteration and hyaline membrane formation. Components of the extrinsic coagulation pathway (*e.g.* tissue factor (TF), thrombin, and fibrin) signal alterations in inflammatory cell traffic and increases in vascular permeability. Procoagulants and fibrin are also thought to promote other key events in the injury including complement activation, production of pro-inflammatory

20   cytokines, inhibition of fibrinolysis, and remodeling of the injured lung. Without wishing to be bound to theory, it is believed that by reducing or blocking these initiating events (extrinsic coagulation) and downstream effects (pro-inflammatory events) in the lungs, disordered fibrin turnover can be reduced or blocked and the evolution of severe structural and functional injury can be reduced or averted during

25   ALI/ARDS. Coagulation blockade can target the TF-Factor VIIa (TF-FVIIa) complex at several points, but the effects of these different strategies on inflammation and the development of lung injury are still being confirmed. The Examples show use of a chimerized monoclonal antibody against human TF (cH36) and its Fab fragment (cH36-Fab) in blocking initiation of coagulation in gram-negative sepsis

30   and prevent acute lung injury.

13

The present invention is intended, in one embodiment, to prevent or treat sepsis and sepsis related conditions (such as DIC, ALI and ARDS) by reducing or blocking activity of a key component of the blood coagulation cascade (*i.e.*, TF). Preferred humanized antibodies, chimeric antibodies, and fragments thereof

5   specifically bind human TF typically to block at least one of FX or Factor IX binding to the TF complex. Typically, such preferred antibodies and fragments also inhibit or block FX or FIX activation of that complex. Thus, the compositions and methods of the invention reduce or block unwanted activation of the blood coagulation cascade by decreasing or preventing activity of a key molecular component.

10

Such preferred antibodies are different from prior antibodies such as those provided by U.S. Pat. No. 6,274,142 ("'142") to O'Brien et al. For instance, the '142 patent reports TF neutralizing antibodies that cannot bind to Factor VII/VIIa or effect proteolysis of Factors IX or X. In contrast, preferred antibodies of the invention

15   substantially reduce or block at least one of FX or FIX binding to the TF complex. See also PCT/US01/07501 (WO 01/70984).

As mentioned previously, unwanted coagulation activation is a prominent feature of certain inflammatory diseases, particularly those associated with

20   autoimmunity. See Weinberg, *et al.*, *Arthritis Rheum.* 34:996-1005 (1991); Kincaid-Smith, *Kidney Int* 7:242-253 (1975); Wakefield, *et al.*, *J Clin Pathol* 47:129-133 (1994); Schoph, *et al.*, *Arch Dermatol Res* 285:305-309 (1993); Zeher, *et al.*, *Clin Immunol Immunopathol* 71:149-155 (1994); More, *et al.*, *J Clin Pathol* 46:703-708 (1993). Elevated TF levels have been reported to be associated with disease activity

25   in systemic lupus erythematosus. See Segal, *et al.*, *J Rheumatol* 27:2827-2832 (2000). It is thus an object of this invention to help control tissue factor-mediated coagulation, thereby reducing or in some instances blocking the inflammation, pathological tissue destruction and undesired remodeling that is a hallmark of many inflammatory diseases.

30

By the phrase "inflammatory disease" including plural forms is meant a pathological condition associated with an unwanted TF-mediated activation of the coagulation. Preferred inflammatory diseases are usually associated with a known or suspected autoimmune condition. Typically, such diseases are further associated with

5   enhanced production of pro-inflammatory cytokines and/or chemokines as determined by standard methods. Examples of such cytokines include IL-1, TNFα, GM-CSF, M-CSF, IL-6, LIF, IL-15, IFNα, and IL12. Examples of such chemokines include IL-8, MIP-1α, MIP-1β, MCP-1, ENA-78, and RANTES. Typically, but not exclusively, one or more of neovascularization and extravascular fibrin deposition is

10   associated with the inflammatory disease. More particular examples of inflammatory diseases according to the invention include arthritis, preferably rheumatoid arthritis (RA); glomerulonephritis, multiple sclerosis, psoriasis, Sjogren's syndrome and inflammatory bowel disease. Arthritis can be readily detected by one or a combination of features including presence of synovial inflammation, pannus

15   formation, and cartilage destruction.

Preferred use of the invention will help reduce, prevent or alleviate symptoms of the inflammatory disease typically by decreasing TF-mediated coagulation activation. Such activation by TF is believed to provide many disadvantages

20   including, but not limited to, supporting the production of inflammatory molecules, enhancing proinflammatory cell activity, increasing tissue destruction, increasing unwanted remodeling and boosting angiogenesis. The invention thus provides a new and fundamental means for addressing inflammatory disease by providing compositions and methods for specifically binding and inhibiting function of TF.

25

Practice of the invention will particularly help in the prevention and treatment of inflammatory autoimmune diseases. Recent work is in agreement with this inventive concept. See Marty, *et al., J Clin Invest* **107**:631-640 (2001); Varisco, *et al., Ann Rheum Dis* **59**:781-787 (2000); Busso, *et al., Arthritis Rheum* **48**:651-659

30   (2003).

As discussed, the U.S. Pat. Nos. 5,986,065 and 6,555,319 to Wong, H. *et al.* and PCT/US98/04644 (WO 98/40408) disclose a variety of murine anti-TF antibodies and antigen binding fragments with good human TF binding characteristics. Such

5   antibodies and fragments can be employed in accord with the present invention. Additionally, such antibodies and fragments can be used to treat experimentally induced sepsis, for instance, in a relevant rodent model. However, and as will be appreciated, such murine antibodies and fragments are not usually appropriate for use in other mammals such as primates and especially human subjects. Further suitable

10   antibodies and fragments are disclosed by U.S. Patent Application Publication No. 20030082636; WO 03/037911 and WO 98/40408.

By the phrase "antigen binding fragment" is meant at least a part of an antibody that specifically binds antigen. An example of such a fragment includes an

15   antibody V domain. Examples of a suitable V domain binding partner include a C domain and acceptable fragments thereof. Further suitable fragments include parts of the V domain having a combined molecular mass for the V domain of between from about 15 kilodaltons to about 40 kilodaltons, preferably between from about 20 kilodaltons to about 30 kilodaltons, more preferably about 25 kilodaltons as

20   determined by a variety of standard methods including SDS polyacrylamide gel electrophoresis or size exclusion chromatography using appropriately sized marker fragments, mass spectroscopy or amino acid sequence analysis. Further specific antigen binding fragments include Fab, F(v), Fab', F(ab')$_2$ and certain single-chain constructs that include the antibody V domain.

25

Additionally suitable antigen binding fragments include at least part of an antigen binding V domains alone or in combination with a cognate constant (C) domain or fragment thereof ("cognate" is used to denote relationship between two components of the same immunoglobulin heavy (H) or light (L) chain). Typical C

30   domain fragments have a molecular mass of between from about 5 kilodaltons to about 50 kilodaltons, more preferably between from about 10 kilodaltons to about 40

kilodaltons, as determined by a variety of standard methods including SDS polyacrylamide gel electrophoresis or size exclusion chromatography using appropriately sized marker fragments, mass spectroscopy or amino acid sequence analysis. Additionally suitable antigen binding fragments are disclosed below as well

5   as in U.S. Pat. Nos. 5,986,065 and 6,555,319 to Wong, H. *et al.* and PCT/US98/04644 (WO 98/40408). See also U.S. Patent Application Publication No. 20030082636 and the following International Applications: WO 03/037911 and WO 98/40408.

10

As also mentioned, one approach to minimize any potential immunorejection by primate hosts such as human patients is to make a chimeric antibody. By the phrase "chimeric antibody" or related phrase including plural forms is meant antibodies as disclosed herein whose light and heavy chain genes have been

15   constructed, typically by genetic engineering, from immunoglobulin gene segments belonging to different species, usually a primate and preferably a human. For example, the variable (V) domains of the genes from a mouse antibody such as H36 may be joined to human constant (C) domains, such as γ_1, γ_2, γ_3, or γ_4. A typical therapeutic chimeric antibody is thus a hybrid protein consisting of the V or antigen-

20   binding domain from a mouse antibody and the C or effector domain from a human antibody, although other mammalian species may be used. A specifically preferred chimeric antibody for use with the invention is the anti-tissue factor antibody cH36 disclosed below in the Examples.

25   Suitable chimeric antibodies for use with the invention can be made by one or a combination of known strategies. As disclosed in the U.S. Pat. Nos. 5,986,065, 6,555,319 and PCT/US98/04644 (WO 98/40408), a highly useful murine anti-TF antibody can be readily obtained from a variety of sources including the American Type Culture Collection (ATCC, 10801 University Boulevard, Manassas, VA

30   20110). The antibody has been deposited as ATCC Accession No. HB-12255. Alternatively, suitable antibodies can be made *de novo* (as polyclonal or monoclonal

as needed) in accord with procedures disclosed in the U.S. Pat. Nos. 5,986,065 and
6,555,319 for instance.

5   See also U.S. Patent Application Publication No. 20030082636 and the
following International Applications: WO 03/037911 and WO 98/40408.

        The antibody deposited with the ATCC H36 is referred to herein as H36. It is
also referenced as H36.D2 and as H36.D2.B7. The antibody designated as H36 is the
antibody produced by the mother clone, and H36.D2 is obtained from the primary
10   clone, whereas H36.D2.B7 is obtained from the secondary clone. No differences
were observed between the antibody produced by those three clones with respect to
the antibody's ability to inhibit TF or other physical properties. In general usage,
H36 is often used to indicate anti-TF antibody produced by any of these clones or
related cell lines producing the antibody. The mouse-human chimeric version of H36
15   is referred to cH36 (and also as Sunol-cH36). See also the U.S. Pat. No. 5,986,065
and PCT/US98/04644 (WO 98/40408) for more specific information about the H36
antibody.

        A preferred chimeric antibody combines the murine variable domain from a
20   suitable antibody such as H36 and a human constant domain. The manipulation is
usually achieved by using standard nucleic acid recombination techniques. A variety
of types of such chimeric antibodies can be prepared, including e.g. by producing
human variable domain chimeras, in which parts of the variable domains, especially
conserved regions of the antigen-binding domain, are of human origin and only the
25   hypervariable regions are of non-human origin. See S.L. Morrison, *Science*,
229:1202-1207 (1985); Oi *et al., BioTechniques* **4**:214 (1986); Teng *et al., Proc. Natl.
Acad. Sci. U.S.A.*, **80**:7308-7312 (1983); Kozobor *et al., Immunology Today* **4**:72-79
(1983); Olsson *et al., Meth. Enzymol.* **92**:3-16 (1983); U.S. Pat. No. 5,986,065; and
PCT/US98/04644 (WO 98/40408).

30

Nucleic acids encoding the H36 variable and constant regions have been disclosed in the U.S. Pat. No. 5,986,065; and PCT/US98/04644 (WO 98/40408), for example. See also U.S. Patent Application Publication No. 20030082636; WO 03/037911 and WO 98/40408.

5

In one embodiment, the anti-TF chimeric antibody will include a human light chain constant (C) domain i.e., Cκ, Cλ or a fragment thereof. Often, the humanized light chain fragment will have an amino acid length of between from about 80 to about 250 amino acids, preferably between from about 95 to about 235 amino acids,

10   more preferably between from about 104 to about 225 amino acids. The size of the humanized light chain fragment can be determined by a variety of standard methods including SDS polyacrylamide gel electrophoresis or size exclusion chromatography using appropriately sized marker fragments, mass spectroscopy or amino acid sequence analysis.

15

Typically, the chimeric antibody for use in the present methods further includes a human heavy chain variable (V) domain having an amino acid length of between about 80 to about 650 amino acids, preferably between from about 95 to about 540 amino acids, more preferably about 102 to about 527 amino acids as

20   determined e.g., by standard SDS polyacrylamide gel electrophoresis or size exclusion chromatography using appropriately sized marker fragments; mass spectroscopy or amino acid sequence analysis.

Nucleic acid sequence encoding suitable human light chain C and V domains

25   have been reported. See e.g., Kabat et al. in Sequences of Proteins of Immunological Interest Fifth Edition, U.S. Dept. of Health and Human Services, U.S. Government Printing Office (1991) NIH Publication No. 91-3242; and GenBank. See the National Center for Biotechnology Information (NCBI)- Genetic Sequence Data Bank (Genbank) at the National Library of Medicine, 38A, 8N05, Rockville Pike,

30   Bethesda, MD 20894. See Benson, D.A. et al., Nucl. Acids. Res. 25:1 (1997) for a more specific description of Genbank.

Suitable recombinant techniques for use in making the chimeric antibodies and other antibodies and fragments as reported herein have been disclosed. See generally Sambrook *et al.* in *Molecular Cloning: A Laboratory Manual* (2d ed.

5   1989); and Ausubel *et al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, (1989).

For some invention applications in which a minimal immunoresponse against an anti-TF antibody is needed, it will be useful to prepare humanized antibodies. By

10   the phrase "humanized" is meant an immunoglobulin that includes at least one human FR subset, preferably at least two or three of same, more preferably four human FR subsets, and one or more CDRs from a non-human source, usually rodent such as a rat or mouse immunoglobulin. Typically preferred humanized immunoglobulins of the invention will include two or more preferably three CDRs. Constant domains

15   need not be present but are often useful in assisting function of humanized antibodies intended for *in vivo* use. Preferred constant domains, if present, are substantially identical to human immunoglobulin constant domains *i.e.*, at least about 90% identical with regard to the amino acid sequence, preferably at least about 95% identical or greater. Accordingly, nearly all parts of the humanized immunoglobulin,

20   with the possible exception of the CDRs, are preferably substantially identical to corresponding parts of naturally occurring human immunoglobulin sequences.

Methods for determining amino acid sequence identity are standard in the field and include visual inspection as well as computer-assisted approaches using

25   BLAST and FASTA (available from the National Library of Medicine (USA) website). Preferred matching programs for most embodiments are available from website for the international ImMunoGeneTics (IMGT) database and a more preferred matching program for this embodiment is the program called Match which is available in the Kabat database. See Johnson G, Wu T. "Kabat database and its

30   application: Future directions." *Nucleic Acids Res.* **29**:205-206 (2001).

By the phrase "humanized antibody" is meant an antibody that includes a humanized light chain and a humanized heavy chain immunoglobulin. See S.L. Morrison, *supra*; Oi *et al.*, *supra*; Teng *et al.*, *supra*; Kozbor *et al.*, *supra*; Olsson *et al.*, *supra*; and other references cited previously. Accordingly, a "humanized

5   antibody fragment" means a part of that antibody, preferably a part that binds antigen specifically.

The H36 or cH36 antibody can be humanized by one or a combination of approaches as described, for example, in U.S Pat. Nos. 5,766,886; 5,693,762;

10   5,985,279; 5,225,539; EP-A-0239400; 5,985,279 and 5,639,641, or as disclosed in the published U.S. application number 20030190705. See also E. Padlan *Mol. Immunol.* **28**:489 (1991); Jones *et al.*, *Nature* **321**:522-525 (1986); Junghans *et al.*, *supra*; and Roguska, *et al. PNAS (USA)* **91**:969 (1994) for additional information on humanizing antibodies.

15

Particular humanized antibodies and fragments thereof for use with the present invention are disclosed below in the Examples section.

Preferred chimeric antibodies, humanized antibodies, as well as fragments

20   thereof that specifically bind human TF. By the term, "specific binding" or a similar term is meant a molecule disclosed herein which binds another molecule, thereby forming a specific binding pair. However, the molecule does not recognize or bind to other molecules as determined by, *e.g.*, Western blotting ELISA, RIA, mobility shift assay, enzyme-immunoassay, competitive assays, saturation assays or other protein

25   binding assays know in the art. See generally, Sambrook *et al.* in *Molecular Cloning: A Laboratory Manual* (2nd ed. 1989); and Ausubel *et al.*, *supra*; and Harlow and Lane in *Antibodies: A Laboratory Manual* (1988) Cold Spring Harbor, New York for examples of methods for detecting specific binding between molecules.

30   Especially suitable chimeric antibodies, humanized antibodies and fragments for use with the invention will feature at least one of: 1) a dissociation constant (K_d)

for the TF of less than about 0.5 nM; and 2) an affinity constant (K_a) for the TF of less than about 10×10^{10} M^{-1}. Methods of preforming such assays are known in the field and include Enzyme-Linked Immuno-Sorbent Assay (ELISA), Enzyme ImmunoAssay (EIA) radioimmunoassay (RIA) and BIAcore analysis.

5

Additionally suitable antibodies will increase survival time in what is sometimes referred to herein as a "standard *in vivo* septic shock assay". Generally, such an assay involves administering gram-negative bacteria to monkeys to induce sepsis. See Taylor *et al. J. Clin. Invest.* 79:918 (1987). More specifically, a dose of

10   *E. coli* (about 10^{10} CFU/kg) is freshly prepared and administered intravenously to a primate, *e.g.* baboon or rhesus monkey, in a 1-2 hour interval. A control group can receive a saline or PBS injection. The treatment group receives a bolus injection of at least 1 mg/kg antibody, preferably about 10 mg/kg prior to infusion of bacteria *e.g.*, less than about 1 hour before. Control and treatment group monkeys are then

15   monitored for about a week and checked for survival. See the Examples below for more specific information about the standard *in vivo* septic shock assay.

A preferred method of the invention employs a humanized antibody, chimeric antibody or fragment that increases monkey survival time (hours or days) by at least

20   about 2-fold, preferably at least about 3 fold, more preferably at least about 5 fold to 10 fold or more as determined by the standard *in vivo* septic shock assay.

Additionally suitable antibodies for use with the invention can attenuate (reduce presence of at least one of interleukin-6 (IL-6) and interleukin-8 (IL-8) in the

25   plasma of subject mammals after at least about 5 hours following administration of the antibody. Methods for detecting IL-6 and IL-8 and quantifying same from plasma are known and include immunological approaches such as RIA, EIA, ELISA and the like.

30   In one approach, sepsis is induced in a suitable primate such as a monkey and preferably a baboon along lines previously mentioned. Prior to inoculation of control

baboon (with about 10^{10} CFU/kg *E. coli* or saline), the treatment baboons receive a bolus injection of at least 1 mg/kg antibody, preferably about 10 mg/kg prior to infusion of bacteria *e.g.*, less than about 1 hour before injection of the inoculum. Baboon survival and IL-6 and IL-8 levels in plasma are monitored by standard

5   procedures.

In another approach, a sepsis-like condition is induced in a suitable primate, such as baboon, using a model described as a "primed sepsis model" (see Welty-Wolf, K. *et al. Am. J. Respir. Crit. Care Med.* **164**:1988 (2001) and described in

10   further detail in Example 4).

Additionally preferred humanized antibodies, chimeric antibodies and fragments thereof exhibit a blood clotting time of between from about 50 to about 350 seconds as determined by a standard prothrombin (PT) time assay, particularly

15   after about 5 minutes administration of the antibody or fragment to the mammal. An especially useful PT assay has been disclosed in the U.S. Pat. Nos. 5,986,065, 6,555,319 and PCT/US98/04644 (WO 98/40408), for example.

Further preferred antibodies for use in accord with the present invention

20   inhibit platelet deposition by at least about 50% as determined by a standard platelet deposition assay. Methods for performing the assay have been disclosed, *e.g.*, in the pending U.S. Pat. application 10/310,113.

Still further preferred antibodies inhibit collagen-induced arthritis in an

25   experimental mouse model. See Example 5.

"Antibody", "antibody for use with the invention" and like phrases refer to whole immunoglobulin as well as immunologically active fragments which bind a desired antigen. The immunoglobulins and immunologically active (antigen-binding)

30   fragments thereof include an epitope-binding site (*i.e.*, a site or epitope capable of being specifically bound by an antibody recognizing antigen). Exemplary antibody

fragments include, for example, Fab, F(v), Fab', F(ab')₂ fragments, "half molecules" derived by reducing the disulfide bonds of immunoglobulins, single chain immunoglobulins, or other suitable antigen binding fragments (see *e.g.*, Bird *et al.*, *Science*, **242**:423-426 (1988); Huston *et al.*, *PNAS, (USA)*, **85**:5879 (1988); Webber

5   *et al.*, *Mol. Immunol.*, **32**:249 (1995)).

Particular chimeric or humanized antibodies of the present invention can be polyclonal or monoclonal, as needed, and may have, without limitation, an IgG1, IgG2, IgG3 or IgG4 isotype or IgA, IgD, IgE, IgM. An especially preferred antibody

10   for use with the invention has or can be manipulated to have an IgG1 (called "hOAT") or IgG4 (called "hFAT") isotype. Such antibodies can be polyclonal or monoclonal as needed to achieve the objectives of a particular invention embodiment. In some instances, single-chain antibodies such as a humanized single-chain will be preferred.

15

Practice of the invention is applicable to a wide spectrum of mammals. Preferably, the mammal is a primate such as a monkey, chimpanzee, or a baboon. More preferably, the primate is a human patient in need of methods disclosed herein *i.e.*, one that has or is suspected of having sepsis or a sepsis-related condition or an

20   inflammatory disorder or disease.

As discussed above, antibodies of the invention and suitable fragments thereof can be administered to a mammal, preferably a primate such as a human, to prevent or reduce sepsis and related complications. According to one embodiment, such

25   antibodies are used with one or more pharmaceutically acceptable non-toxic carriers such as sterile water or saline, glycols such as polyethylene glycol, oils of vegetable origin, and the like. In particular, biocompatible, biodegradable lactide polymer, lactide glycolide copolymer or polyoxyethylene, polyoxypropylene copolymers may be useful excipients. Other potentially useful administration systems include

30   ethylene vinyl acetate copolymer particles, osmotic pumps, and implantable infusion systems and liposomes. If needed, one or more suitable antibodies or fragments will

be in the form of a solution or suspension (or a lyophilized form that can be
reconstituted to a solution or suspension), and will preferably include approximately
0.01% to 10% (w/w) of the antibody of the present invention, preferably
approximately 0.01% to 5% (w/w) of the antibody.

5

As discussed, the antibody or fragment can be administered according to the
invention as the sole active agent or in combination with other known anti-sepsis
therapies. For instance, such antibodies or fragments can be administered to a human
patient before, during, or after intervention with one or more appropriate antibotics,

10   typically a broad spectrum intravenous antibiotic therapy. Preferred antibiotics
include those known to have broad spectrum anti-microbial activity, covering gram-
positive, gram-negative, and anaerobic bacteria. Thus in one embodiment, such
antibiotics are given during or after administration of the antibodies and fragments
disclosed herein, preferably parenterally in doses adequate to achieve bactericidal

15   serum levels. After stabilizing the patient, various recognized supportive therapies
can be used to assist recovery such as administration of oxygen, intravenous fluids,
and medications that increase blood pressure. Dialysis may be necessary in the event
of kidney failure, and mechanical ventilation is often required if respiratory failure
occurs.

20

Persons "at risk" for developing sepsis and related conditions include, but are
not limited to, the very old and very young individuals. Also at risk are those with
challenged immune systems such as patients infected with a DNA or RNA virus such
as HIV or herpes. Nearly any bacterial organism can cause sepsis. Certain fungi and

25   (rarely) viruses may faciliate sepsis and related conditions. Generally, toxins released
by the bacteria or fungus may cause direct organ (*e.g.*, lung, kidney) or tissue
damage, and may lead to low blood pressure and/or poor organ function. These
toxins also produce a vigorous inflammatory response from the body which
contributes to septic shock.

30

25

Additional risk factors include underlying illnesses, such as diabetes; hematologic cancers (lymphoma or leukemia); and other malignancies and diseases of the genitourinary system, liver or biliary system, and intestinal system. Other risk factors are recent infection, prolonged antibiotic therapy, and having been exposed to

5   a recent invasive surgical or medical procedure. Symptoms of sepsis and related conditions are known in the field and include, but are not limited to, fever, chills, lightheadedness, shortness of breath, palpitations, cool and/or pale extremities, fever, agitation, lethargy, and confusion.

10   Success of the invention in the prevention or treatment of sepsis and related conditions can be evaluated by the caregiver using one or a combination of approaches. Typically, a reduction or elimination of one or more of the foregoing symptoms can be taken as indicative that the sepsis or related condition has been addressed. Preferably, patients receiving such treatment will survive at least about 2

15   fold longer than patients who do not receive such intervention.

As discussed, the invention provides a method for reducing cytokine production in a mammal *e.g.*, by administering to the mammal a therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment

20   thereof that binds specifically to tissue factor (TF) to form a complex. Preferably, Factor X or Factor IX binding to the complex is inhibited and the administration is sufficient to reduce the cytokine production in the mammal. Suitable humanized antibodies, chimeric antibodies and fragments thereof are disclosed herein. Acceptable methods for monitoring cytokine production in a mammal are known and

25   include specific methods outlined in the Examples section.

Therapeutic antibodies and fragments in accord with the invention can be used in parenteral or intravenous administration, particularly in the form of liquid

30   solutions. Such compositions may be conveniently administered in unit dose and may be prepared in accordance with methods known in the pharmaceutical art. See

Remington's Pharmaceutical Sciences, (Mack Publishing Co., Easton PA, (1980)).
By the term "unit dose" is meant a therapeutic composition of the present invention
employed in a physically discrete unit suitable as unitary dosages for a primate such
as a human, each unit containing a pre-determined quantity of active material

5   calculated to produce the desired therapeutic effect in association with the required
diluent or carrier. The unit dose will depend on a variety of factors including the type
and severity of sepsis to be treated, general health of the individual, medical history,
and the like. Precise amounts of the antibody to be administered typically will be
guided by judgment of the practitioner, however, the unit dose will generally depend

10   on the route of administration and be in the range of 10 ng/kg body weight to 50
mg/kg body weight per day, more typically in the range of 100 ng/kg body weight to
about 10 mg/kg body weight per day. Suitable regimens for initial administration in
booster shots are also variable but are typified by an initial administration followed
by repeated doses at one or more hour intervals by a subsequent injection or other

15   administration. Alternatively, continuous or intermittent intravenous infusions may
be made sufficient to maintain concentrations of at least from about 10 nanomolar to
10 micromolar of the antibody (or suitable fragment) in the blood.

       Antibodies and fragments for use with the invention are preferably
20   substantially pure when used in the disclosed methods and assays. References to an
antibody being "substantially pure" mean an antibody or protein that has been
separated from components which naturally accompany it. For example, by using
standard immunoaffinity or protein A affinity purification techniques, an antibody of
the invention can be purified from hybridoma or cell culture medium by using native

25   TF as an antigen or protein A resin. Similarly, native TF can be obtained in
substantially pure form by using an antibody of the invention with standard
immunoaffinity purification techniques. Particularly, an antibody or protein is
substantially pure when at least 50% of the total protein (weight % of total protein in
a given sample) is an antibody or protein of the invention. Preferably the antibody or

30   protein is at least 60 weight % of the total protein, more preferably at least 75 weight
%, even more preferably at least 90 weight %, and most preferably at least 98 weight

% of the total material. Purity can be readily assayed by known methods such as SDS polyacrylamide gel electrophoresis (PAGE), column chromatography (*e.g.*, affinity chromatography, size exclusion chromatography), mass spectroscopy or HPLC analysis. Preferably, the antibodies and fragments will be used in a sterile

5   format.

The molecular weight of the antibodies of the invention will vary depending on several factors such as the intended use and whether the antibody includes a conjugated or recombinantly fused toxin, pharmaceutical, radioisotope or detectable

10   label or the like. Also the molecular weight will vary depending on nature and extent of post-translational modifications if any (such as glycosylation) to the antibody. The modifications are a function of the host used for expression with *E. coli* producing non-glycosylated antibodies and eucaryotic hosts, such as mammalian cells or plants, producing glycosylated antibodies. In general, an antibody of the invention will have

15   a molecular weight of between approximately 20 to 150kDa. Such molecular weights can be readily determined by molecular sizing methods such as SDS-PAGE followed by protein staining or Western blot analysis.

It will be apparent that the foregoing method for making the humanized cH36

20   antibody can be readily adapted to make other humanized antibodies and antigen binding fragments according to the invention.

A. Preparation Of Humanized Anti-Tissue Factor Binding Antibody

25   Preparation and use of a humanized anti-tissue factor binding antibody is described. See also Examples 1-3 below.

Briefly, preferred antibodies bind human tissue factor to form a binding complex. The tissue factor may be naturally occurring or recombinant human (rhTF).

30   Preferably, factor X or factor IX binding to the complex is inhibited. In a preferred invention embodiment, the humanized antibody has an apparent affinity constant (K_A,

28

M^{-1}) for the hTF of less than about 1 nM, preferably less than about 0.5 nM, more

preferably between from about 0.01 nM to about 0.4 nM. See Examples 1-3, below

for more information about determining affinity constants for the humanized

antibodies. By "specific binding" is meant that the humanized antibodies form a

5   detectable binding complex with the TF (or rhTF) and no other antigen as determined

by standard immunological techniques such as RIA, Western blot or ELISA.

More preferred humanized anti-TF binding antibodies made in accord with

this invention exhibit an apparent affinity constant (K_A, M^{-1}) for native human TF of

10   at least about 1 x 10^8 M^{-1} as determined by surface plasmon analysis (particularly,

BIACore analysis in accordance with the procedures of Example 3 which follows),

more preferably at least about 5 x 10^8 M^{-1} as determined by surface plasmon analysis,

still more preferably an apparent affinity constant (K_A, M^{-1}) for native human TF of

at least about 3 x 10^9 M^{-1} as determined by surface plasmon resonance analysis. Such

15   substantial binding affinity of antibodies of the invention contrast sharply from much

lower binding affinities of previously reported antibodies.

The nucleic acid (SEQ ID NOS. 1 and 3) and amino acid (SEQ ID NOS. 2

and 4) sequences of a particular tissue factor binding antibody that has been

20   humanized by the present methods *i.e.* H36.D2.B7. See Figures 1A and 1B of the

drawings and the PCT application WO 98/40408, for instance. SEQ ID NOS. 1 and 2

are the nucleic acid and amino acid respectively of the light chain variable domain,

and SEQ ID NOS. 3 and 4 are the nucleic acid and amino acid respectively of the

heavy chain variable domain, with hypervariable regions (CDRs or Complementarity

25   Determining Regions) underlined in all of those sequences.

Additional tissue factor binding humanized antibodies of the invention will

have substantial amino acid sequence identity to either one or both of the light chain

or heavy sequences shown in Figures 1A and 1B. More particularly, such antibodies

30   include those that have at least about 70 percent homology (amino acid sequence

identity) to SEQ ID NOS. 2 and/or 4, more preferably about 80 percent or more

homology to SEQ ID NOS. 2 and/or 4, still more preferably about 85, 90 or 95 percent or more homology to SEQ ID NOS. 2 and/or 4.

5   More particular tissue factor binding humanized antibodies of the invention will have high amino acid sequence identity to hypervariable regions (shown with double underlining in Figures 1A and 1B) of SEQ ID NOS. 2 and 4). Specific antibodies will have one, two or three hypervariable regions of a light chain variable domain that has high sequence identity (at least 90% or 95% amino acid sequence identity) to or be the same as one, two or three of the corresponding hypervariable

10   regions of the light chain variable domain of H36.D2.B7 (those hypervariable regions shown with underlining in Figure 1A and are the following:

     1) LASQTID (SEQ ID NO. 5);

     2) AATNLAD (SEQ ID NO. 6); and

     3) QQVYSSPFT (SEQ ID NO. 7).

15

Additionally specific antibodies that have been humanized by the methods described herein and bind tissue factor will have one, two or three hypervariable regions of a heavy chain variable domain that have high sequence identity (at least 90% or 95% amino acid sequence identity) to or be the same as one, two or three of

20   the corresponding hypervariable regions of the heavy chain variable domain of H36.D2.B7 (those hypervariable regions shown with underlining in Figure 1B and are the following:

     1) TDYNVY (SEQ ID NO. 8);

     2) YIDPYNGITIYDQNFKG (SEQ ID NO. 9); and

25   3) DVTTALDF (SEQ ID NO. 10).

Certain nucleic acids encoding some or all of the antibodies or fragments disclosed herein will preferably have a length sufficient (preferably at least about 100, 200 or 250 base pairs) to bind to the sequence of SEQ ID NO. 1 and/or SEQ ID

30   NO. 3 under the following moderately stringent conditions (referred to herein as "normal stringency" conditions): use of a hybridization buffer comprising 20%

formamide in 0.9M saline/0.12M sodium citrate (6xSSC) buffer at a temperature of 37°C and remaining bound when subject to washing once with that 2xSSC buffer at 37°C.

5   More specifically, certain of the nucleic acids (preferably at least about 100, 200 or 250 base pairs) will bind to the sequence of SEQ ID NO. 1 and/or SEQ ID NO. 3 under the following highly stringent conditions (referred to herein as "high stringency" conditions): use of a hybridization buffer comprising 20% formamide in 0.9M saline/0.12M sodium citrate (6xSSC) buffer at a temperature of 42°C and

10   remaining bound when subject to washing twice with that 1xSSC buffer at 42°C.

          Suitable nucleic acids preferably comprise at least 20 base pairs, more preferably at least about 50 base pairs, and still more preferably a nucleic acid of the invention comprises at least about 100, 200, 250 or 300 base pairs.

15

          Generally preferred nucleic acids of the invention will express an antibody of the invention that exhibits the preferred binding affinities and other properties as disclosed herein. See also the U.S. Pat. No. 5,986,065 and PCT/US98/04644 (WO 98/40408) for more information.

20

          Other appropriate nucleic acids will have substantial sequence identity to either one or both of the light chain or heavy sequences shown in Figures 1A and 1B. More particularly, preferred nucleic acids will comprise a sequence that has at least about 70 percent homology (nucleotide sequence identity) to SEQ ID NOS. 1 and/or

25   3, more preferably about 80 percent or more homology to SEQ ID NOS. 1 and/or 3, still more preferably about 85, 90 or 95 percent or more homology to SEQ ID NOS. 1 and/or 3.

          Additionally specific nucleic acid sequences will have high sequence identity

30   to hypervariable regions (shown with underlining in Figures 1A and 1B) of SEQ ID NOS. 1 and 3). Such nucleic acids include those that code for an antibody light chain

variable domain and have one, two or three sequences that code for hypervariable regions and have high sequence identity (at least 90% or 95% nucleotide sequence identity) to or be the same as one, two or three of the sequences coding for corresponding hypervariable regions of H36.D2.B7 (those hypervariable regions

5   shown with underlining in Figure 1A and are the following:

1) CTGGCAAGTCAGACCATTGAT (SEQ ID NO: 11);

2) GCTGCCACCAACTTGGCAGAT (SEQ ID NO: 12); and

3) CAACAAGTTTACAGTTCTCCATTCACGT (SEQ ID NO: 13).

10   More specific nucleic acids also code for an antibody heavy chain variable domain and have one, two or three sequences that code for hypervariable regions and have high sequence identity (at least 90% or 95% sequence identity) to or be the same as one, two or three of the sequences coding for corresponding hypervariable regions of H36.D2.B7 (those hypervariable regions shown with underlining in Figure 1B and

15   are the following:

1) ACTGACTACAACGTGTAC (SEQ ID NO. 14);

2)
TATATTGATCCTTACAATGGTATTACTATCTACGACCAGAACTTCA
AGGGC (SEQ ID NO. 15); and

20   3) GATGTGACTACGGCCCTTGACTTC (SEQ ID NO. 16).

More specific humanized antibodies for use with the methods of this invention that bind TF are those in which each of framework regions (FRs) 1, 2, 3 and 4 has at least about 90% amino acid sequence identity, preferably at least about

25   95% or greater identity to the light chain FR sequences shown in Figure 3A (SEQ ID NO. [ ]), preferably, the sequence shown as "LC-09" in Figure 3A. Additionally specific humanized antibodies include a light chain constant domain having at least about 90% amino acid sequence identity, preferably at least about 95% sequence identity or greater to the sequence shown in Figure 5A (SEQ ID NO. [ ]) or Figure

30   6A (SEQ ID NO. [ ]).

Further specific humanized antibodies are those in which each of framework regions (FRs) 1, 2, 3 and 4 has at least about 90% amino acid sequence identity, preferably about 95% identity or greater to the heavy chain sequences shown in Figure 4A (SEQ ID NO. ___), preferably, the sequence shown as "HC-08" in Figure

5   4A. Additional humanized antibodies have a heavy chain constant domain with at least about 90% amino acid sequence identity, preferably at least about 95% identity or greater, to sequence shown in Figure 5B (SEQ ID NO. ___) or Figure 6B (SEQ ID NO. ___).

10   In certain embodiments, the humanized antibody will have an IgG1 (hOAT) or IgG4 (hFAT) isotype as disclosed in the published U.S. application number 20030190705.

Also provided by the present invention are functional fragments of the

15   humanized antibodies disclosed herein. Examples of such fragments include, but are not limited to, those that bind TF with an affinity constant (Kd) of less than about 1 nM, preferably less than about 0.5 nM, more preferably between from about 0.01 nM to about 0.4 nM. Specifically preferred are antigen binding Fab, Fab', and F(ab)₂ fragments.

20

As discussed, the invention features humanized antibodies that include at least one murine complementarity determining region (CDR), e.g., CDR1, CDR2, CDR3. In one invention embodiment, the antibodies bind specifically to human tissue factor (TF) to form a complex. Typically, the factor X or factor IX binding to TF or TF-

25   FVIIa and activation by TF-FVIIa thereto is inhibited. As mentioned above, preferred CDRs (light and heavy chain) are from a rodent source, typically the mouse.

In one embodiment of the humanized antibodies of the invention, the

30   antibodies further include at least one human framework region (FR) subset. Preferably, all the FRs (light and heavy chains) are human.

In a more particular embodiment, the first CDR (CDR1) of the heavy chain
hypervariable region that binds human TF is at least 90% identical to the CDR1
amino acid sequence shown in Figure 4B (SEQ ID NO. ___), preferably at least about
5   95% identical or greater to that sequence. Typically, the second CDR (CDR2) of the
heavy chain hypervariable region is at least 90% identical to the CDR2 amino acid
sequence shown in Figure 4C (SEQ ID NO. ___), preferably at least about 95%
identical or greater. Preferably also, the third CDR (CDR3) of the heavy chain
hypervariable region is at least 90% identical to the CDR3 sequence shown in Figure
10   4D (SEQ ID NO. ___), more preferably about 95% identical or greater to that
sequence.

In another invention embodiment, the first CDR (CDR1) of the light chain
hypervariable region that binds human TF is at least 90% identical to the CDR1
15   amino acid sequence shown in Figure 3B (SEQ ID NO. ___), preferably at least about
95% identical or greater. Typically, the second CDR (CDR2) of the light chain
hypervariable region is at least 90% identical to the CDR2 amino acid sequence
shown in Figure 3C (SEQ ID NO. ___), preferably about 95% identical or greater.
Preferably, the third CDR (CDR3) of the light chain hypervariable region is at least
20   90% identical to the CDR3 amino acid sequence shown in Figure 3D (SEQ ID NO.
___), more preferably about 95% identical or greater to that sequence. ·

Additional humanized antibodies suitable for use with the present methods
include a first framework region (FR1) of the heavy chain hypervariable region that
25   binds human TF which FR1 is at least 90% identical to the amino acid sequence
shown in Figure 4A (SEQ ID NO. ___) as "FR1 HC-08", preferably about 95%
identical or greater to that sequence. In one embodiment, the FR1 comprises at least
one of the following amino acid changes: E1 to Q; Q5 to V; P9 to G; L11 to V; V12
to K; Q19 to R; and T24 to A. Preferably, the FR1 includes two, three, four, five, or
30   six of those changes with all of those amino acid changes being preferred for many
applications.

Further humanized antibodies suitably bind human TF and include a second framework region (FR2) of the heavy chain hypervariable region which FR2 is at least 90% identical to the sequence shown in Figure 4A (SEQ ID NO. ▓) as "FR2

5   HC-08", preferably about 95% identical or greater to that sequence. In one embodiment, the FR2 at least one of the following amino acid changes: H41 to P and S44 to G. A preferred FR2 includes both of those amino acid changes.

The invention also features use of humanized antibodies that bind human TF

10   in which a third framework region (FR3) of the heavy chain hypervariable region is at least 90% identical to the sequence shown in Figure 4A (SEQ ID NO. ▓) as "FR3 HC-08", preferably about 95% identical or greater to that sequence. In one embodiment, the FR3 includes at least one of the following amino acid changes: S76 to T; T77 to S; F80 to Y; H82 to E; N84 to S; T87 to R; D89 to E and S91 to T. A

15   preferred FR3 includes two, three, four, five or six of those amino acid changes with all seven of those amino acid changes being generally preferred.

Also featured is use of humanized antibodies that suitably bind human TF and in which the fourth framework region (FR4) of the heavy chain hypervariable region

20   is at least 90% identical to the amino acid sequence shown in Figure 4A (SEQ ID No. ▓) as "FR4 HC-08", preferably at least about 95% identical or greater to that sequence. Preferably, the FR4 includes the following amino acid change: L113 to V.

Additional humanized antibodies bind human TF and also feature a first

25   framework region (FR1) of the light chain hypervariable region which is at least about 90% identical to the amino acid sequence shown in Figure 3A (SEQ ID NO. ▓) as "FR1 LC-09", preferably at least about 95% identical or greater to that sequence. In one embodiment, the FR1 comprises at least one of the following amino acid changes: Q11 to L; L15 to V; E17 to D; and S18 to R. A preferred FR1

30   includes two or three of such amino acid changes with all four amino acid changes being generally preferred.

35

The present invention also features use of humanized antibodies that bind human TF and in which a second framework region (FR2) of the light chain hypervariable region is at least about 90% identical to the amino acid sequence shown in Figure 3A (SEQ ID NO. ___) as "FR2 LC-09", preferably at least about 95% identical or greater to that sequence. A preferred FR2 has the following amino acid change: Q37 to L.

Also encompassed by the invention is use of particular humanized antibodies that bind human TF in which a third framework region (FR3) of the light chain hypervariable region is at least about 90% identical to the amino acid sequence shown in Figure 3A (SEQ ID NO. ___) as "FR3 LC-09", preferably at least about 95% identical or greater to that sequence. In one embodiment, the FR3 has at least one of the following amino acid changes: K70 to D, K74 to T, A80 to P, V84 to A, and N85 to T. Preferably, the FR3 has two, three, or four of such amino acid changes with all five of the changes being generally preferred.

Additional humanized antibodies appropriate for use with the methods disclosed herein bind TF and include a fourth framework region (FR4) of the light chain hypervariable region which FR4 is at least about 90% identical to the sequence shown in Figure 3A (SEQ ID NO. ___) as "FR4 LC-09", preferably at least about 95% identical or greater to that sequence. In one embodiment, the FR4 includes at least one and preferably all of the following amino acid changes: A100 to Q and L106 to I.

The invention also features a human TF binding fragment of the foregoing humanized antibodies. Examples of such fragments include Fab, Fab', and F(ab)$_2$. See the published U.S. application number 20030190705 and references cited therein for additionally preferred humanized anti-TF antibodies made in accord with this invention.

The following three nucleic acid vectors pSUN36 (humanized anti-TF antibody Ig G1-HC expression vector), pSUN37 (humanized anti-TF antibody Ig G4-HC expression vector), and pSUN38 (humanized anti-TF antibody LC expression vector) have been deposited pursuant to the Budapest Treaty with the American Type

5   Culture Collection (ATCC) at 10801 University Boulevard, Manassas VA 20110-2209. The vectors were assigned the following Accession Numbers: PTA-3727 (pSUN36); PTA-3728 (pSUN37); and PTA-3729 (pSUN38).

Suitable expression and purification strategies for making and using the

10   humanized anti-TF antibodies of this invention have been disclosed in the published U.S. application number 20030190705, for instance.

As discussed, the invention also provides useful kits for performing one or more of the methods provided herein. In one embodiment, the kit includes at least

15   one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to human tissue factor (TF) to form a complex, wherein factor X or factor IX binding to the complex is inhibited. Typically also, the humanized antibody, chimeric antibody, or fragment thereof is provided in a pharmaceutically acceptable vehicle such as saline, water or buffer. The kit may include a pharmaceutically

20   acceptable vehicle for dissolving the humanized antibody, chimeric antibody or fragment prior to use.

The following non-limiting examples are illustrative of the invention. In the following examples and elsewhere the method of the invention is applied to the

25   humanization of the murine anti-tissue factor antibody H36. See the U.S Patent Nos. 5,986,065 and 6,555,319; U.S. Patent Application Publication No. 20030082636; WO 03/037911 and WO 98/40408, and the published U.S. patent application number 20030190705 and references cited therein as well as the discussion above. Sometimes, the Fab fragment of H36 or cH36 will be referred to as "H36-Fab" and

30   "cH36-Fab", respectively, for the sake of convenience.

All documents mentioned herein are fully incorporated by reference in their entirety.

EXAMPLE 1 – Humanization of Anti-Tissue Factor Antibody

5   The description of how to make and use a particular murine antibody called H36.D2 (sometimes also called H36 as discussed above) is described in U.S. Pat. Nos. 5,986,065 and 6,555,319. The present example shows how to make and use a humanized version of that antibody. A humanized H36 antibody has a variety of uses including helping to minimize potential for human anti-mouse antibody (HAMA)

10   immunological responses. These and other undesired responses pose problems for use of the H36 antibody in human therapeutic applications.

          A. Preparation of chimeric anti-tissue factor antibody (cH36)

15   The H36 antibody described previously is an IgG2a murine antibody. H36 was first converted to a mouse-human chimeric antibody for clinical development. To do this, the heavy and light chain genes for H36 were cloned (see U.S. Patent No. 5,986,065). The heavy chain variable domain was fused to a human IgG4 constant (Fc) domain and the light chain variable domain was fused to a human kappa light

20   chain constant domain. The resulting IgG4κ chimeric antibody was designated cH36 (and is also referred to as Sunol-cH36). For multiple uses of H36 or cH36 in patients with chronic diseases, a fully humanized cH36 is preferred so that it will decease or eliminate any human anti-chimeric antibody (HACA) immunological response. The humanization of cH36 is described below.

25

          B. Humanization Strategy for cH36 Antibody

          Humanization of the chimeric anti-tissue factor antibody cH36 was achieved by using a "FR best-fit" method of the invention. This method takes full advantage

30   of the fact that a great number of human IgGs with known amino acid sequences or sequences of human IgG fragments are available in the public database. The

sequences of the individual framework regions of the mouse heavy and light variable

domains in cH36 are compared with the sequences respective heavy or light chain

variable domains or human frameworks (or fragments thereof) in the Kabat database

(see *e.g.*, Kabat *et al.* in *Sequences of Proteins of Immunological Interest* Fifth

5   Edition, U.S. Dept. of Health and Human Services, U.S. Government Printing Office

(1991) NIH Publication No. 91-3242 or http://immuno.bme.nwu.edu). The following

criteria were used to select the desired human IgG framework region subsets for

humanization: (1) The number of mismatched amino acids was kept as low as

possible. (2) Amino acids inside the "vernier" zone (amino acids in this zone may

10   adjust CDR structure and fine-tune the fit to antigen, see Foote, J. and Winter, G., *J.*

of Mol. Bio. **224(2)**:487-499 [1992]) were left unchanged. (3) Conservative amino

acid substitutions were favored when evaluating similar candidates. The matching

program used for this comparison can be found in Kabat database. See Johnson G,

Wu T. "Kabat database and its application: Future directions." *Nucleic Acids Res.*

15   **29**:205-206 (2001). The program finds and aligns regions of homologies between the

mouse sequences and human sequences in the Kabat's database. By using this unique

FR best-fit method, it is anticipated that the humanized LC or HC variable domains

of the target IgG may have all the four FRs derived from as few as one human IgG

molecule or to as many as four different human IgG molecules.

20

B(i). Selection of Human IgG Kappa Light Chain Variable Domain

Framework Regions

The amino acid sequence in each of the framework regions of cH36 LC was

25   compared with the amino acid sequence in the FRs in human IgG kappa light chain

variable domain in Kabat Database. The best-fit FR was selected based on the three

criteria described above.

The amino acid sequence of human IgG kappa light chain variable domain

30   with a Kabat Database ID No. 005191 was selected for humanization of cH36 LC

FR1. The amino acid sequence of human IgG kappa light chain variable domain with a Kabat Database ID No. 019308 was selected for humanization of cH36 LC FR2. The following mutations were made in cH36 LC FR1 to match the amino acid sequence of a human IgG kappa light chain variable domain with a Kabat Database

5   ID No. 005191: Q11 → L, L15 → V, E17 → D, S18 → R. One mutation Q37 → L was made cH36 LC FR2 to match the amino acid sequence of a human IgG kappa light chain variable domain with a Kabat Database ID No. 019308 (see Table 1A for sequence information).

10   The amino acid sequence of a human IgG kappa light chain variable domain with a Kabat Database ID No. 038233 was selected for humanization of cH36 LC FR3. The amino acid sequence of a human IgG kappa light chain variable domain with a Kabat Database ID No. 004733 was selected for humanization of cH36 LC FR4. The following mutations were made in cH36 LC FR3 to match the amino acid

15   sequence of a human IgG kappa light chain variable region with a Kabat Database ID No. 038233: K70 → D, K74 → T, A80 → P, V84 → A, N85 → T. Two mutations A100 → Q and L106 → I were made cH36 LC FR4 to match the amino acid sequence of a human IgG kappa light chain variable domain with a Kabat Database ID No. 004733 (see Table 1B for sequence information).

20
          B(ii). Selection of Human IgG Heavy Chain Variable Domain Framework Regions

          The amino acid sequence in each of the framework regions of cH36 HC was
25   compared with the amino acid sequence in the FRs in human IgG heavy chain variable domain in Kabat Database. The best-fit FR was selected based on the three criteria described above.

          The amino acid sequence of a human IgG heavy chain variable domain with a
30   Kabat Database ID No. 000042 was selected for humanization of cH36 HC FR1. The amino acid sequence of a human IgG heavy chain variable domain with a Kabat

40

Database ID No. 023960 was selected for humanization of cH36 HC FR2. The following mutations were made in cH36 HC FR1 to match the amino acid sequence of a human IgG heavy chain variable domain with a Kabat Database ID No. 000042: E1 → Q, Q5 → V, P9 → G, L11 → V, V12 → K, Q19 → R, T24 → A. Two mutations H41 → P and S44 → G were made cH36 HC FR2 to match the amino acid sequence of a human IgG heavy chain variable domain with a Kabat Database ID No. 023960 (see Table 2A for sequence information).

The amino acid sequence of a human IgG heavy chain variable domain with a Kabat Database ID No. 037010 was selected for humanization of cH36 HC FR3. The amino acid sequence of a human IgG heavy chain variable domain with a Kabat Database ID No. 000049 was selected for humanization of cH36 HC FR4. The following mutations were made in cH36 HC FR3 to match the amino acid sequence of a human IgG heavy chain variable domain with a Kabat Database ID No. 037010: S76 → T, T77 → S, F80 → Y, H82 → E, N84 → S, T87 → R, D89 → E, S91 → T. One mutations L113 → V was made cH36 HC FR2 to match the amino acid sequence of a human IgG heavy chain variable domain with a Kabat Database ID No. 000049 (see Table 2B for sequence information).

Table 1. Comparison of cH36 and Human Light Chain (LC) FR Sequences

Table 1A

Names	LC-FR1 (23 aa)	LC-FR2 (15 aa)
cH36-LC	1 10 20 DIQMTQSPASQSASLGESVTITC	35 49 WYQQKPGKSPQLLIY
Human-LC	L V DR 005191	L 019308

Table 1B

Names	LC-FR3 (32 aa)	LC-FR4 (10 aa)
cH36-LC	57 60 70 80 88 98 107 GVPSRFSGSGSGTKFSFKISSLQAEDFVNYYC	FGAGTKLELK
Human-LC	D T P AT 038233	Q I 004733

Table 2. Comparison of cH36 and Human Heavy Chain (HC) FR Sequences

Table 2A

Names	HC-FR1 (30 aa)	HC-FR2 (14 aa)
cH36-HC	49 1 10 20 30 36 EIQLQQSGPELVKPGASVQVSCKTSGYSFT WVRQSHGKSLEWIG	
Human-HC	Q V G VK R A 000042	P G 023960

Table 2B

Names	HC-FR3 (32 aa)	HC-FR4 (11 aa)
cH36-HC	67 75 85 95 107 117 KATLTVDKSSTTAFMHLNSLTSDDSAVYFCAR	WGQGTTLTVSS
Human-HC	TS Y E S R E T 037010	V 000049

Once the decisions on the desired human framework regions were made, the following three techniques were used to achieve the desired amino acid substitutions in both the light and heavy chains: (1) Regular PCR was used for cloning, to introduce cloning or diagnostic restriction endonuclease sites, and to change amino acid residues located at the ends of the variable domains. (2) PCR-based mutagenesis

was used to change multiple amino acid residues at a time, especially when these residues were in the middle of the variable domains. (3) Site-directed mutagenesis was used to introduce one or two amino acid substitutions at a time. Site-directed mutagenesis was done following the protocol described in Stratagene's

5   "QuickChange Site-Directed Mutagenesis Kit" (Catalog #200518).

After each step, the partially humanized clones were sequenced and some of these variable domains were later cloned into expression vectors. The plasmid tKMC180 was used to express LC mutants, and the pJRS 355 or pLAM 356 vector

10   was used to express HC mutants as IgG1 or IgG4, respectively. Some of these clones were then combined and expressed transiently in COS cells to determine the expression levels by ELISA.

The final fully humanized forms of the anti-TF heavy and light variable

15   domains were cloned into what is sometimes referred to herein as a "mega vector" and transfected into CHO and NSO cells for IgG expression. Stable cell lines were then used to produce amounts of humanized anti-TF sufficient for analysis. The resulting humanized versions are 100% human in origin (when the CDR sequences are not considered). The humanized IgG4 kappa version is designated hFAT

20   (humanized IgG Four Anti-Tissue Factor antibody) and the IgG1 kappa version is designated hOAT (humanized IgG One Anti-Tissue Factor antibody). These fully humanized versions of cH36 are intended for treating chronic indications, such as thrombosis, cancer and inflammatory diseases.

25   C. Generation of Humanized Anti-TF Antibody Heavy Chain

        1. PCR amplification and cloning into pGem T-easy of anti-TF mAb cH36
            heavy chain (HC) variable domain were performed using plasmid
            pJAIgG4TF.A8 (an expression vector for chimeric H36) as template and
30   primers TFHC1s2 and TFHC1as2. Primer TFHC1s2 introduced a *BsiW*1 site
            upstream of the initiation codon and also an amino acid change E1 to Q in

framework (FR) 1. Primer TFHC1as introduced an amino acid change **L113** to V in FR4. This step resulted in the construct **HC01.**

2. PCR-based mutagenesis using the previous construct (HC01) and the following four primers generated construct **HC02.** Upstream PCR used primers TFHC1s2 and TFHC7as. Downstream PCR used primers TFHC7s and TFHC1as2. PCR using upstream and downstream PCR products as templates and with primers TFHC1s2 and TFHC1as2 yielded **HC02.** The use of primers TFHC7s and TFHC7as introduced two amino acid changes in FR2: **H41** to P and **S44** to G.

3. PCR-based mutagenesis using HC02 as template and the following four primers generated construct **HC03.** Upstream PCR used primers TFHC1s2 and TFHC5as2. Downstream PCR used primers TFHC5s and TFHC1as2. PCR using upstream and downstream PCR products as templates and with primers TFHC1s2 and TFHC1as2 yielded **HC03.** The use of primers TFHC5s and TFHC5as2 introduced three amino acid changes in FR3: **T87** to R, **D89** to E, and **S91** to T. A *Bgl* II site was also introduced at position. 87.

4. PCR amplification was performed using primers TFHC2s and TFHC3as and HC03 in pGem as template. TFHC2s sits upstream of the cloning site in pGem. TFHC3as sits in framework 3 and introduces two amino acid changes in FR3: **H82** to E and **N84** to S. The resulting PCR band was cloned into pGem and then the proper size insert was digested with *BsiW*1 and *Bgl* II. Cloning of this fragment into **HC03** yields **HC04.**

5. PCR-based mutagenesis using **HC04** as template and the following primers resulted in **HC05.** Upstream PCR used primers TFHC1s2 and TFHC6as. Downstream PCR used primers TFHC6s and TFHC1as2. Mutagenic PCR using upstream and downstream PCR products as templates and with primers

TFHC1s2 and TFHC1as2 yielded **HC05**. This step introduced the following amino acid changes in FR3: **S76** to T, **T77** to S, and **F80** toY.

6. PCR-based mutagenesis using **HC05** as template and the following four primers generated **HC06**. Upstream PCR used primers TFHC2s and TFHC2as2. Downstream PCR used primers TFHC3s2 and TFHC1as2. Amplification using TFHC2as2 introduced an amino acid change in FR1: **P9** to G. Primer TFHC3s2 changes **Q19** to R and **T24** to A. PCR using upstream and downstream PCR products as template and with primers TFHC1s2 and TFHC1as2 yielded **HC06.**

7. A point mutation from I to M in position 2 of FR1 was spontaneously introduced during construction of **HC06**. PCR amplification using **HC06** as template and TFHC1s3 and TFHC1as2 as primers, corrected this erroneous substitution and also introduced an amino acid. change in FR1: **Q5** to V. The resulting construct was **HC07**.

8. Construct **HC08** was made by PCR-based mutagenesis using **HC07** as template and the following primers. TFHC2s and TFHC2as3 were used for the upstream product. The downstream product was previously amplified using TFHC1s3 and TFHC1as2 (see step 7). The use of primer TFHC2as3 introduced two amino acid changes in FR1: **L11** to V and **V12** to K. A spontaneous point mutation resulted in a phenylalanine to leucine (F → L) change at position 64 in CDR2. Further screening and sequencing yielded construct **HC08R1**, which has the correct sequence of F at position 64 in CDR2.

9. Two constructs, **HC11** and **HC12**, were generated by site-directed mutagenesis from **HC07**. Two complementary primers TFHC8sP and TFHC8asP were used along with **HC07** as template to produce **HC11** which contains three amino acid changes in FR1: G9 to P, L11 to V, and V12 to K.

Then, **HC11** was methylated and column purified for the next round of site directed mutagenesis. PCR using **HC11** as a template and the complementary primers TFHC9sL and TFHC0asL generated **HC12** which has a mutation from **V11** to L in FR1.

10. Construct **HC09** was derived from **HC12** by performing PCR using **HC12** as a template and the complementary primers TFHC10sK and TFHC10asK. **HC09** contains an amino acid change: **K12** to V in FR1.

11. Construct **HC10** was made from **HC09**. PCR using **HC09** as a template and the complementary primers LV-1 and LV-2 resulted in the generation of **HC10**, which contains a mutation from **L11** to V in FR1.

After each mutation step, the partially humanized or fully humanized clones were sequenced and some of these variable domains were later cloned into expression vectors. pJRS 355 or pLAM 356 vector was used to express HC mutants fused to Fc of human IgG1 or IgG4.

Figures 3A-D summarize steps 1-11 and shows incremental amino acid changes introduced into FR1-4. Except HC08, all other heavy chain mutants and cH36 contain F at position 64 in CDR2. HC08 has a mutation from F to L at position 64. Figures 4B-D show the heavy chain CDR sequences.

Primers Used for Heavy Chain Humanization

TFHC1s2
5' TTTCGTACGTCTTGTCCCAGATCCAGCTGCAGCAGTC 3'

TFHC1as2
5' AGCGAATTCTGAGGAGACTGTGACAGTGGTGCCTTGGCCCCAG 3'

TFHC7s
5' GTGAGGCAGAGCCCTGGAAAGGGCCTTGAGTGGATTGG 3'

TFHC7as

5' CCAATCCACTCAAGGCCCTTTCCAGGGCTCTGCCTCAC 3'

TFHC5s
5'GCATCTCAACAGCCTGAGATCTGAAGACACTGCAGTTTATTTCTGTG 3'

5

TFHC5as2
5' CTGCAGTGTCTTCAGATCTCAGGCTGTTGAGATGCATGAAGGC 3'

TFHC3as
10   5' GTCTTCAGATCTCAGGCTGCTGAGCTCCATGAAGGCTGTGGTG 3'

TFHC2s
5' TACGACTCACTATAGGGCGAATTGG 3'

15   TFHC6s
5' CTGTTGACAAGTCTACCAGCACAGCCTACATGGAGCTCAGCAG 3'

TFHC6as
5' CTGCTGAGCTCCATGTAGGCTGTGCTGGTAGACTTGTCAACAG 3'

20
TFHC2as2
5' GCACTGAAGCCCCAGGCTTCACCAGCTCACCTCCAGACTGCTGCAGC 3'

TFHC3s2
25   5'CTGGGGCTTCAGTGCGGGTATCCTGCAAGGCTTCTGGTTACTCATTCAC
3'

TFHC1s3
5' TCGTACGTCTTGTCCCAGATCCAGCTGGTGCAGTCTGGAGGTGAGC 3'

30
TFHC2as3
5' GCACTGAAGCCCCAGGCTTCTTCACCTCACCTCCAGACTGCACC 3'

TFHC9sL
35   5' GCAGTCTGGACCTGAGCTGAAGAAGCCTGGGG 3'

TFHC9asL
5' CCCCAGGCTTCTTCAGCTCAGGTCCAGACTGC 3'

40   TFHC8sP
5' GCTGGTGCAGTCTGGACCTGAGGTGAAGAAGCC 3'

TFHC8asP
5' GGCTTCTTCACCTCAGGTCCAGACTGCACCAGC3'

45
TFHC10sK

47

5' GCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTC 3'

TFHC10asK
5' GAAGCCCCAGGCTTCACCAGCTCAGGTCCAGACTGC 3'

5

LV-1
5' CAGTCTGGACCTGAGGTGGTGAAGCCTGGG 3'

LV-2
10   5' CCCAGGCTTCACCACCTCAGGTCCAGACTG 3'

D.   Generation of Humanized Anti-TF Antibody Light Chain

15   1. PCR amplification was performed using plasmid pJAIgG4TF.A8 (an expression
         vector for chimeric H36) as template and primers TFLC1s2.1 and TFLC1as2.
         This step introduced a cloning site, *Age*I, upstream of the coding region. It also
         introduced the **L106I** mutation in FR4. This step yielded the construct **LC03**.

20   2. Site-directed mutagenesis was performed using complementary primers TFLC5s
         and TFLC5as and LC03 as template. This step introduced the mutation **Q37L** in
         FR2 and added a *Pst*I site for diagnostic purposes. This new construct is named
         LC04.

25   3. PCR amplification was performed using **LC04** as template and primers TFHC2s
         and TFLC2as1. This step generated **Fragment A** that will be used in step 6. This
         step introduced **Q11L** and **L15V** mutations in FR1.

     4. PCR amplification was performed using **LC04** as template and primers
30   TFLC1s2.1 and TFLC1asR. This introduced the *Kpn*I site at the end of LC
         variable domain. Cloning of this PCR fragment into pGEM yields **pGEM04K**
         that will be used in step 6.

     5. PCR amplification was performed using **LC04** as template and primers TFLC2s
35   and TFLC4as. This step generated **Fragment C** that will be used in step 6.

Three mutations **E17D, S18R** in FR1 and **A100Q** in FR4 were introduced in this step.

6. PCR-based mutagenesis using **Fragment A** and **Fragment C** as templates and primers TFHC2s and TFLC4as yielded **Fragment D**. Cloning of **Fragment D** into pGEM04K yielded the construct **LC05**.

7. PCR amplification was performed using pGEM04K as template and primers TFLC1s2.1 and TFLC4as. This step generated **Fragment H**, which is then cloned into pGEM04K. This introduced the **A100Q** mutation in FR4 and the construct is named **LC06**.

8. PCR amplification was performed using **LC06** as template and primers TFLC1s2.1 and TFLC3as. This step generated **Fragment I** that will be used in step 10. This introduced the **K70D** and the **K74T** mutations in FR3.

9. PCR amplification was performed using **LC06** as template and primers TFLC3s2 and TFLC4as. This step generated **Fragment F** that will be used in step 10. This introduced the **A80P** mutation in FR3.

10. PCR using **Fragment I** and **Fragment F** as templates and primers TFLC1s2.1 and TFLC4as yielded **Fragment J**. Cloning of **Fragment J** into pGEM yielded the construct **LC07**.

11. Site-directed mutagenesis was conduced using complementary primers TFLC08sds and TFLC08sdsa and **LC07** as template. This step introduced the mutations **V84A** and **N85T** in FR3. This construct is named **LC08**.

12. The *Age*I to *Eco*O109I fragment from **LC05** containing the mutations **Q11L, L15V, E17D, S18R** and **Q37L** is cloned into **LC08**. This yielded the construct **LC09**.

13. Site-directed mutagenesis was conduced using **LC09** as template and the
complementary primers LC105 and LC103. This step introduced the **T85N**
mutation in FR3 and yielded the construct **LC10**.

5

14. Site-directed mutagenesis was conducted using **LC10** as template and the
complementary primers LC115 and LC113. This step introduced the **D70K**
mutation in FR3. This yielded the construct **LC11**.

10   15. Site-directed mutagenesis was conducted using **LC11** as template and the
complementary primers LC125a and LC123a. This step introduced the **K42Q**
mutation in FR2. This yielded the construct **LC12**.

After each mutation step, the partially humanized or fully humanized LC clones
15   were sequenced and some of these variable domains were later cloned into expression
vector tKMC180.

<u>Oligonucleotide Primers Used for Light Chain Humanization</u>

20   TFLC1as2:
5' TTCGAAAAGTGTACTTACGTTTGATCTCCAGCTTGGTCCCAG 3'

TFLC1s2.1:
5' ACCGGTGATATCCAGATGACCCAGTCTCC 3'
25
TFLC5s:
5' GGTTAGCATGGTATCTGCAGAAACCAGGG 3'

TFLC5as:
30   5' CCCTGGTTTCTGCAGATACCATGCTAACC 3'

TFHC2s:
5' TACGACTCACTATAGGGCGAATTGG 3'

35   TFLC2as1:
5' CCACAGATGCAGACAGGGAGGCAGGAGACTG 3'

TFLC1asR:
5'
TTCGAAAAGTGTACTTACGTTTGATCTCCAGCTTGGTACCAGCACCGAAC
G 3'

5

TFLC2s:
5' CCTGTCTGCATCTGTGGGAGATAGGGTCACCATCACATGC 3'

TFLC4as:
10 5' GATCTCCAGCTTGGTACCCTGACCGAACGTGAATGG 3'

TFLC3as:
5' GTAGGCTGCTGATCGTGAAAGAAAGTCTGTGCCAGATCC 3'

15 TFLC3s2:
5' CACGATCAGCAGCCTACAGCCTGAAGATTTTGTAAATTATTACTGTC 3'

TFLC08sds:
5' GCAGCCTACAGCCTGAAGATTTTGCAACTTATTACTGTCAACAAG 3'

20

TFLC08sdsa:
5' CTTGTTGACAGTAATAAGTTGCAAAATCTTCAGGCTGTAGGCTGC 3'

LC105:
25 5' CAGCAGCCTACAGCCTGAAGATTTTGCAAATTATTACTGTCAAC 3'

LC103:
5' GTTGACAGTAATAATTTGCAAAATCTTCAGGCTGTAGGCTGCTG 3'

30 LC115:
5' CAGTGGATCTGGCACAAAGTTTTCTTTCACGATCAGCAGC 3'

LC113:
5' GCTGCTGATCGTGAAAGAAACTTTGTGCCAGATCCACTG 3'

35

LC125a:
5' CTGCAGAACCAGGGCAATCTCCTCAGCTCCTG 3'

LC123a:
40 5' CAGGAGCTGAGGAGATTGCCCTGGTTTCTGCAG 3'

Figure 5A shows the sequence of the human kappa light chain constant

domain (SEQ ID NO. ____) . Figure 5B shows the human IgG1 heavy chain

51

constant domain (SEQ ID NO. ___). Figure 6A shows the hFAT (IgG4) constant
domain sequence (SEQ ID NO. ____). Figure 6B provides the human IgG4 heavy
chain constant domain (SEQ ID NO. ___). See also the published U.S. patent
application number 20030190705 and references cited therein for additional
5   disclosure relating to the foregoing immunoglobulin constant domain sequences.

     EXAMPLE 2 – Expression and Purification of Humanized anti-TF Antibodies

10   The partially humanized or fully humanized LC and HC clones were cloned
     into expression vectors. The plasmid tKMC18 was used to express LC mutants fused
     to human kappa chain, and pJRS 355 or pLAM 356 vector was used to express HC
     mutants fused to Fc of human IgG1 or IgG4. Some combinations of the HC and LC
     clones were then co-transfected into COS cells. The transiently expressed IgGs in
15   COS cells were assayed for the whole IgG production and binding to TF by ELISA.
     For disclosure relating to these particular vectors see the published U.S. patent
     application number 20030190705 and references cited therein.

             The final fully humanized forms of the anti-TF heavy and light variable
20   domains (combination of HC08 and LC09) were cloned into what is referred to as a
     Mega expression vector (pSUN34, see Figure 2) and transfected into CHO and NSO
     cells for IgG expression. Stably transfected cell lines producing the IgG4κ or IgG1κ
     humanized anti-TF antibody were cloned. The selected stable cell lines were then
     used to produce amounts of humanized anti-TF sufficient for analysis. The resulting
25   humanized versions are approximately 100% human in origin (when the CDR
     sequences are not considered). The humanized IgG4 kappa version (produced by
     pSUN35) is designated hFAT (humanized IgG Four Anti-Tissue Factor antibody) and
     the IgG1 kappa version (produced by pSUN34) is designated hOAT (humanized IgG
     One Anti-Tissue Factor antibody). These fully humanized versions of cH36 are
30   intended for treating chronic indications, such as cancer and inflammatory diseases.

One of the NSO cell lines (OAT-NSO-P10A7) that expresses (combination of HC08 and LC09) was thawed and extended in 10 mL of IMDM medium supplemented with 10% FBS in a 15 mL tube and centrifuged. The cell pellet was resuspended in 10 mL of fresh media and passed to a T25 flask and incubated at 37°C

5   in 5% CO_2. In order to prepare a sufficient number of cells to inoculate a hollow fiber bioreactor, the cells were expanded to obtain a total of $6x10^8$ cells. A bioreactor was set up as per manufacturer's instruction manual. The harvested cells were pelleted and resuspended in 60 mL of IMDM containing 35% FBS and injected into the extracapillary space of the bioreactor. Concentrations of glucose and lactate were

10   monitored daily and the harvest material was centrifuged and pooled. The harvested material was tested for anti-TF antibody concentrations by ELISA assay. The pooled sample containing anti-TF antibody (hFAT) were then purified and analyzed as described below.

15   A. rProtein A Sepharose Fast Flow Chromatography

Recombinant humanized anti-TF monoclonal antibody consists of two light and two heavy chains. Heavy chain is a fusion of mouse variable domain (unaltered or humanized as described above) and human IgG1 or IgG4 Fc domain, while light

20   chain contains mouse variable domain (unaltered or humanized as described above) and human κ domain. It is well established that human IgG Fc region has high affinity for Protein A or recombinant Protein A (rProtein A).

Harvest pools containing humanized anti-TF antibody (hFAT) were adjusted

25   to pH 8.0 ± 0.1 by adding 0.08 ml of 1 M Tris-HCl, pH 8.0 per ml of sample. Then the sample is filtered through low protein-binding 0.22 micron filters (e.g., Nalgene sterile disposable tissue culture filter units with polyethersulfone membrane from Nalge Nunc International, Cat. No. 167-0020). Following sample application, rProtein A column (from Pharmacia) is washed with 5 bed volumes of 20 mM Tris-

30   HCl, pH 8.0 to remove unbound materials such as media proteins. Since the harvest medium contains high content of bovine serum, a stepwise pH gradient wash was

used to remove bovine IgG from the column. The stepwise pH gradient was achieved by increasing the relative percentage of Buffer B (100 mM acetic acid) in Buffer A (100 mM sodium acetate). A typical pH stepwise wash employed 20%, 40%, and 60% Buffer B. Elute the column with 100% Buffer B and collect fractions based on

5   A_{280}. The pooled fractions were adjusted to pH 8.5 with addition of 1 M Tris base.

B. Q Sepharose Fast Flow Chromatography

Anion ion exchange chromatography is very effective in separating proteins

10   according to their charges. The eluted and pH-adjusted sample from rProtein A column was diluted with two volumes of water, and the pH is checked and adjusted to 8.5. The sample was then loaded to a 5 ml (1.6 x 2.5 cm) Q Sepharose Fast Flow equilibrated with 20 mM Tris-HCl, pH 8.5 and the column washed with (1) 5 bed volumes of 20 mM Tris-HCl, pH 8.5; and (2) 4 bed volumes of 20 mM Tris-HCl, pH

15   8.5 containing 100 mM NaCl. The IgG protein was then eluted with bed volumes of 20 mM Tris-HCl, pH 8.5 containing 500 mM NaCl. The protein peaks were pooled and buffer-exchanged into PBS using ultrafiltration device.

20   **EXAMPLE 3**: Septic Shock Model in Rhesus Monkeys

In this model, septic shock was induced by infusion of live *E. coli*, a gram-negative bacterium (see Taylor *et al.*, J. Clin. Invest. **79**:918-825 (1987)) in rhesus monkeys. The shock induced by *E. coli* causes activation both coagulation and

25   inflammation, ultimately leading to death. The ability of an anti-TF antibody of the present invention to prolong the survival times of rhesus monkeys treated with live *E. coli* was examined using the rhesus model of septic shock described by Taylor *et al.*, *supra*. Rhesus monkeys weighing 3-5 kilograms were fasted overnight before study and immobilized the morning of the experiment with ketamine hydrochloride (14

30   mg/kg, intramuscularly). Sodium pentobarbital was then administered in the cephalic vein through a percutaneous catheter to maintain a light level of surgical anesthesia (2 mg/kg initially and with additional amounts approximately every 20 to 45 minutes for

6 hours). A femoral vein was exposed aseptically and cannulated in one hind limb for sampling blood and administering gentamicin. Gentamicin was administrated by means of 30-minute intravenous infusions. An infusion of 9 mg/kg was administrated at the end of *E. coli* infusion (t = 2 hours). An infusion of 4.5 mg/kg

5   was administrated 6 hours after *E. coli* infusion. Additional gentamicin (4.5 mg/kg, i.m.) was administrated once daily after day 1 for 3 more days. Each monkey was placed on its side in contact with controlled-temperature heating pads and rectal temperature was monitored. Animals were intubated orally and allowed to breathe spontaneously.

10

The *E. coli* strain 086:K61H (ATCC 33985) was freshly prepared in less than 12 hours prior to injection. Each monkey received a 2-hour intravenous infusion of *E. coli* at a dose of 4 x 10^{10} CFU/kg. Control group monkeys received PBS 30 minutes before infusion of *E. coli*. Treatment group monkeys received a bolus (2-3

15   minutes) dose of anti-tissue factor antibody (cH36, diluted in PBS if necessary) 30 minutes before infusion of *E. coli* (see Timeline for injection schedule). The percutaneous catheter was used to infuse *E. coli*, PBS and anti-TF antibody.

Timeline for anti-TF antibody and *E. coli* administration.

All monkeys were monitored continuously for 8 hours and observed daily for a maximum of 7 days, for the following: survival time: monitored and recorded hourly; temperature was measured and recorded hourly for the first 8 hours and then once a day for up to 7 days.

Blood samples were collected at the following time points: T = -0.5*, 0**, 1, 2, 4, 6, 24 hours as shown in Table 3 for the analysis of hematological references and inflammatory cytokines. (*T = -0.5, right before injection of cH36 or saline control; **T = 0, right before infusion of *E coli* but 30 min after injection of cH36 or saline control).

Table 3. The schedule for collecting blood samples.

Time Point	*Hematology*	*Plasma for Analysis*
Day 1; t = -0.5 hr (just prior to test article or vehicle infusion)	X	X
Day 1; t = 0 hour (30 minutes after treatment, just prior to *E. coli* infusion)	X	X
Day 1; 1 hour (following *E. coli* infusion	X	X
Day 1; 2 hour (following *E. coli* infusion)	X	X
Day 1; 4 hour (following *E. coli* infusion)	X	X
Day 1; 6 hour (following *E. coli* infusion)	X	X
Day 1; 24 hour (following *E. coli* infusion)	X	X
Volume of whole blood / time point	1.0 mL	1.8 mL
Anticoagulant	EDTA	Sodium Citrate

The results of this study are shown in Table 4 and Fig.7A-D. Anti-TF antibody cH36 protected rhesus monkeys very well from *E. coli*-induced septic shock when administered as a10 mg/kg bolus injected intravenously (Table 4), while attenuating inflammatory cytokines IL-8 and IL-1β, and to a lesser extent IL-6 and TNF-α (Fig. 7A-D).

Table 4. Protective Effect of cH36 on *E coli*-induced Septic Shock in Rhesus Monkeys

Treatment	Weight (kg)	Sex	Survival Time (hr)	Average Survival Time (hr)
Saline	3.6	F	8	16
	4.5	M	24	
Sunol-cH36 (10 mg/kg)	3.1	F	>168	>111
	4.0	M	54	

EXAMPLE 4: Acute Lung Injury Model in Baboons

A. Acute lung injury is an important cause of morbidity and mortality in sepsis. Patients infected with gram-negative sepsis have a high incidence of acute respiratory distress syndrome and multiple organ failure. It has been shown that blocking tissue factor function with active site-inactivated factor VIIa could limit

sepsis-induced acute lung injury and other organ damage in baboons (see Welty-Wolf, K. *et al., Am. J. Respir. Crit. Care Med.* 164:1988 (2001)). A critical pathophysiological feature of the acute respiratory distress syndrome (ARDS) is local activation of extrinsic coagulation and inhibition of fibrinolysis. As the injury

5   evolves, these perturbations cause deposition of fibrin in the microvascular, interstitial and alveolar spaces of the lung leading to capillary obliteration and hyaline membrane formation. Components of the extrinsic coagulation pathway such as TF, thrombin and fibrin signal alterations in inflammatory cell traffic and increases in vascular permeability. Procoagulants and fibrin also promote other key events in the

10   injury including complement activation, production of proinflammatory cytokines, inhibition of fibrinolysis, and remodeling of the injured lung. It has been established that sepsis-induced TF expression activates the extrinsic coagulation cascade in the lung and leads to a procoagulant environment, which results in fibrin deposition and potentiates inflammation. By blockade of the initiating events of extrinsic

15   coagulation, their effects on proinflammatory events in the lungs and disordered fibrin turnover may be corrected and the evolution of severe structural and functional injury may be averted during experimental ARDS. Recent studies demonstrated that preventing initiation of coagulation at TF-Factor VIIa complex with active site inhibited factor VIIa (FVIIai) or TF pathway inhibitor (TFPI) attenuates fibrin

20   deposition and inflammation in sepsis, thereby limiting acute lung injury (ALI) and other organ damage in baboons.

A model for sepsis-induced ALI model has been established in baboons. See Welty-Wolf, K. *et al., Am. J. Respir. Crit. Care Med.* **164**:1988 (2001). In this

25   model, hyperdynamic cardiovascular and systemic inflammatory responses are pre-activated by a priming infusion of killed *E. coli*. After 12 hours, a second dose of live *E. coli* is given to the animals to induce pulmonary and renal failure similar to humans with sepsis and ARDS. Using this model, blockade of TF function by FVIIai and TFPI was shown to attenuate systemic inflammatory responses, decrease fibrin

30   deposition in tissues, and prevented lung and renal injury.

In this model, overnight fasted, adult baboons (*Papio cyanocephalus*) were sedated with intramuscular ketamine (20-25 mg/kg) and intubated. Heavy sedation was maintained with ketamine (3-10 mg/kg/h) and diazepam (0.4-0.8 mg/kg every 2 hours). Animals were mechanically ventilated (21% O_2) with a volume-cycled

5   ventilator and paralyzed intermittently with pancuronium (4 mg intravenously) before respiratory measurements. An indwelling arterial line and a pulmonary artery catheter were placed via femoral cut down for hemodynamic monitoring. All animals received approximately 10^9 CFU/kg heat-killed *E. coli* 086:K61H (ATCC 33985) as a 60 min infusion at t = 0 h, 12 h before live *E. coli*. Sepsis was induced at t = 12 h by

10 infusing 10^{10} CFU/kg of live *E. coli* in a volume of 50 mL over 60 min. Gentamicin (3 mg/kg i.v.) and Ceftazidime (1 gm i.v.) were administered 60 min after completion of the live *E. coli* infusion. Fluids were given as needed to maintain pulmonary capillary wedge pressure (PCWP) at 8-12 mmHg and to support blood pressure. Dopamine was used for hypotension when mean arterial pressure (MAP) fell below

15 65 mmHg despite fluids. After 48 h (36 h after the live bacteria infusion) animals were deeply anesthetized and killed by KCl injection. Physiologic parameters including heart rate (HR), temperature, arterial blood pressure, pulmonary artery pressure, ventilator parameters, and fluid intake were recorded every hour. Measurements were obtained every six hours of cardiac output (CO) by

20 thermodilution, central venous pressure (CVP), PCWP, arterial and mixed venous blood gases, oxygen saturation, oxygen content and hemoglobin (Hgb) as reported. Urinary catheter output was measured every six hours and fluid balance calculated as total i.v. fluid intake minus urine output.

25   Treatment efficacy for each intervention were assessed by comparing the responses of drug-treated animals with vehicle-treated animals using the physiological, histologic, and biochemical endpoints of lung injury listed below:

   • Physiological endpoints were evaluated as the alveolar-to-arterial O_2 difference
     (AaDo2), pulmonary system compliance (C_L), pulmonary artery pressures,

30   pulmonary vascular resistance (PVR) and tissue W/D ratios. Secondary

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endpoints were fluid volume requirements, serum HCO_3, V_E at constant $PaCO_2$, urine output, creatinine, and systemic DO_2, VO_2 and VCO_2.

- Pathologic endpoints analyzed were gross tissue appearance and qualitative light microscopic analysis, including fibrin deposition, in lung, kidney, adrenal, and other tissues.

- Biochemical endpoints were tissue myeloperoxidase (MPO) levels, total tissue and lavage protein, and lavage LDH. Lung and small bowel edema were measured by wet/dry weights.

Blood samples were drawn at 0, 12, 13, 18, 24, 36, and 48 h. Plasma (from citrated blood) and serum were separated and stored at -80° C. Plasma samples were assayed for interleukin (IL) 6 and IL 8 using ELISA kits (R and D Systems, Inc., Minneapolis, MN).

The experimental protocol is summarized in Table 5.

Table 5. Experimental Protocol

Time (hours)	0	6	12	14	18	24	30	36	42	48		
Heat-killed *E. coli*	X											
Live *E. coli*			X									
Antibiotics				X								
Vehicle or drug				X	X	X	X	X	X	X		
Studies*	X	X	X	X	X	X	X	X	X	X		
Sacrifice										X		
*Studies include serum, plasma, urine and physiology measurements outlined in the detailed methods.												

TF blockade was done using a total antibody dose of 3.5 mg/kg for the cH36
Fab and 5.25 mg/kg for cH36. The intravenous loading dose of test article (1.8
5   mg/kg for cH36 Fab or 2.7 mg/kg for cH36) was begun 2 hours after infusion of live
microorganisms, at the time antibiotics were administered, followed by a constant 34-
hour infusion of 50 mcg/kg per hour for cH36 Fab or 75 mcg/kg/hour for cH36.

Table 6. Experimental Design

Group	Treatment	# Animals
1	Sepsis + vehicle	5
2	Sepsis + cH36 Fab (3.5 mg/kg total, 1.8 mg/kg loading, 50 mcg/kg/hr infusion for 34 hr)	2
3	Sepsis + Sunol-cH36 (5.25 mg/kg total, 2.7 mg/kg loading, 75 mcg/kg/hr infusion for 34 hr)	5

10

TF blockade with bolus injection of cH36, followed by infusion, attenuated systemic
expression of the proinflammatory cytokine IL-8 and IL-6 to a lesser extent (Figs. 11A-B),
and provided partial renal and lung protection in baboons challenged with *E. coli*. Interim
15   analysis indicates that cH36 administration attenuates increases in mean pulmonary artery
pressure, lung system compliance (Figs. 8A-B) and in the alveolar-arterial oxygen gradient.
The kidneys in the animals examined thus far appeared grossly normal at necropsy, the

kidney myeloperoxidase levels remained lower (Figure 9A) and urine output was maintained throughout the experiments. The small bowel wet/dry ratio in the treated animals was significantly lower that in the control animals indicative of less edema in the cH36 treated animals (Figure 9B).

5

These data indicate that coagulation blockade targeting TF with Sunol-cH36 prevents inflammation and the development of organ injury in gram-negative sepsis. These data also show, for the first time, a new strategy for management of ARDS in humans with anticoagulant.

10

B. The following data further show that cH36 and cH36-Fab are useful in preventing lung injury in septic baboons.

Briefly, the objective of this part of the example is to further confirm effects of Sunol-cH36 and cH36-Fab on procoagulant-fibrinolytic balance and inflammation in the

15   lung and relate them to the structural and gas exchange abnormalities in ALI in an experimental sepsis model in baboons. See section A, above.

All baboons (*Papio cyanocephalus*) were mechanically ventilated (21% O_2), anesthetized, and given a dose of heat-killed *E. coli* (1 x 10^9 CFU/kg) intravenously 12 hours prior to the onset of live *E. coli* sepsis (1-2 x 10^{10} CFU/kg). The study design consisted of

20   three groups of baboons as shown in Table 7, below. The baboons in the first group (n=6) were administered vehicle (PBS) and served as controls. The animals in the second group (n=3) were injected with cH36-Fab (3.5 mg/kg total, 1.8 mg/kg bolus loading dose followed by constant infusion of 50 mcg/kg/hr for 34 hours). The third group (n=6) received cH36 (5.25 mg/kg total, 2.7 mg/kg bolus loading dose followed by a constant infusion of 75

25   mcg/kg/hr for 34 hours). The intravenous loading dose of drug (1.8 mg/kg for cH36-Fab or 2.7 mg/kg for cH36) was started 2 hours after infusion of live microorganisms (at the 14-hour time point) followed by a constant infusion of 50 mcg/kg per hour for cH36-Fab or 75 mcg/kg/hour for cH36 until the end of the experiment at 48 hours. Antibiotics were administered at the 14-hour time point. Treatment efficacy was assessed by comparison of

30   the responses of the treated animals with the controls using physiological, histological and biochemical parameters of lung injury.

Table 7.   Experimental Design

Group	Treatment	No. of Baboons
1	Sepsis + vehicle	6
2	Sepsis + cH36-Fab (3.5 mg/kg total, 1.8 mg/kg loading, 50 mcg/kg/hr infusion for 34 hr)	3
3	Sepsis + cH36 (5.25 mg/kg total, 2.7 mg/kg loading, 75 mcg/kg/hr infusion for 34 hr)	6

From the foregoing data, it can be concluded that animals treated with cH36 had a less hyperdynamic systemic response to sepsis.

The following Materials and Methods were used as needed to conduct the experiments in this Example. They were also used elsewhere in this disclosure as indicated.

C. Materials and Methods

Mechanically ventilated (21% O_2), anesthetized baboons (*Papio cyanocephalus*) were given a dose of heat-killed *E. coli* (1×10^9 CFU/kg) intravenously 12 hours prior to the onset of live *E. coli* sepsis ($1-2 \times 10^{10}$ CFU/kg). The intravenous loading dose of drug (1.8 mg/kg for cH36-Fab or 2.7 mg/kg for cH36) was started 2 hours after infusion of live microorganisms (14 hours), at the time antibiotics were administered, followed by a constant infusion of 50 mcg/kg per hour for cH36-Fab or 75 mcg/kg/hour for cH36. The total antibody dose was 3.5 mg/kg for the cH36-Fab and 5.25 mg/kg for cH36. Treatment was initiated after the onset of gram-negative sepsis because we have previously shown that TF blockade is effective as a rescue strategy. Because initial studies suggested greater efficacy and no harmful effects of whole antibody compared to Fab, comparisons were made between untreated sepsis controls and septic animals treated with cH36 whole antibody. Experimental groups are as shown in Table 7. Statistical analyses used ANOVA for physiologic data and t test or Mann Whitney U for biochemical and BAL data. Data are expressed as mean ± sem and p values are shown.

Animals were handled in accordance with appropriate guidelines. The animals were divided randomly into treatment and sepsis control groups. After an overnight fast, each animal was sedated with intramuscular ketamine (20-25 mg/kg) and intubated. Heavy sedation was maintained with ketamine (3-10 mg/kg/h) and

5   diazepam (0.4-0.8 mg/kg every 2 hours). Animals were ventilated with a volume-cycled ventilator and paralyzed intermittently with pancuronium (4 mg intravenously) before respiratory measurements. The FiO_2 was 0.21, tidal volume 12 ml/kg, positive end-expiratory pressure 2.5 cm H_2O, and a rate adjusted to maintain an arterial PCO_2 of 40 mmHg. An indwelling arterial line and a pulmonary artery catheter were

10   placed via femoral cut down for hemodynamic monitoring. The animals received gentamicin sulfate (3 mg/kg iv) and ceftazidime (1 gm iv) two hours after the start of live *E. coli* infusion (14 hours). The animals were supported with intravenous volume infusion (Ringer's lactate) at a rate sufficient to maintain the pulmonary capillary wedge pressure (PCWP) at 8 to 12 mmHg. Dopamine was used if needed to maintain

15   mean arterial pressure of 60 mmHg. After 48 h (36 h after the live bacteria infusion) animals were deeply anesthetized and killed by KCl injection. Predefined early termination criteria included refractory hypotension (MAP less than 60 mmHg despite dopamine and adequate PCWP), hypoxemia (need for FIO_2 greater than 40%), or refractory metabolic acidosis (pH < 7.10 with normal $PaCO_2$). The

20   experimental protocol was the same as that shown in Table 5, above.

Physiological parameters including heart rate (HR), temperature, arterial blood pressure, pulmonary artery pressure, ventilator parameters, and fluid intake were recorded every hour. Measurements were obtained every six hours of cardiac

25   output (CO) by thermodilution, central venous pressure (CVP), PCWP, arterial and mixed venous blood gases, oxygen saturation, oxygen content and hemoglobin (Hgb). Urinary catheter output was measured every six hours and fluid balance calculated as total iv. fluid intake minus urine output.

30   Blood samples were drawn at 0, 12, 13, 18, 24, 36, and 48 h. Complete blood

counts were performed on whole blood (Sysmex-1000 Hemocytometer; Sysmex, Inc., Long Grove, IL). Plasma (from citrated blood) and serum were separated and stored at −80°C. Fibrinogen was measured using an ST4 mechanical coagulation analyzer (Diagnostica Stago, Parsippany, NJ). Prothrombin time (PT) and activated partial

5   thromboplastin time (aPTT) were measured in duplicate, and antithrombin III (ATIII) activity was measured on an MDA coagulation analyzer (Organon Teknika, Durham, NC) with a chromogenic assay and expressed as % of the kit standard. ELISA was used to measure plasma thrombin-antithrombin (TAT) complexes (Dade Behring, Deerfield, IL) in plasma and BAL. cH36 and cH36-Fab levels in blood and BAL

10   were measured by Sunol Molecular (Miramar, FL). Serum samples were assayed for interleukin 1β (IL-1β), IL-6, IL-8, and TNF receptor-1 (TNFR-1) using ELISA kits (R and D Systems, Inc., Minneapolis, MN). Blood creatinine was measured with standard clinical techniques.

15   Tissues were collected at autopsy as follows: After the experiments the thorax was opened, the left mainstem bronchus ligated, and the left lung removed. BAL was performed on the left upper lobe with 240 mL 0.9% saline. Samples of lung tissue from the left lower lobe were manually inflated and immersed in 4% paraformaldehyde for light microscopy. Four samples were taken at random from the

20   remainder of the left lung for wet/dry weight determination taking care to avoid large vascular and bronchial structures. Additional samples from lung, kidney, liver, small bowel, heart, and adrenal were flash frozen in liquid nitrogen and stored at −80°C. The entire right lung was inflation-fixed for 15 min at 30 cm fixative pressure with 2% glutaraldehyde in 0.85 M Na cacodylate buffer (pH 7.4). Additional tissue from

25   kidney, liver, small bowel, heart, and adrenal was fixed by immersion in 4% paraformaldehye. Four samples of small bowel were selected randomly for wet/dry weight determination.

30   Myeloperoxidase (MPO) activity and protein concentration of lung homogenates and protein and lactate dehydrogenase (LDH) concentrations of BAL

fluid were measured as described (*Am J Resp Crit Care Med* 1998;157:938). MPO activity was expressed as a change in absorbance/min/g wet weight tissue. LDH values were expressed in units of activity per liter (U/L).

5   An important objective of the following Examples was to determine the effects of cH36 and cH36-Fab on procoagulant-fibrinolytic balance and inflammation in the lung. It was also an objective to correlate these parameters to the structural and gas exchange abnormalities in ALI in an experimental sepsis model in baboons.

10   **D. Results:** Treatment with cH36 prevents fibrinogen depletion in baboons with *E. coli* sepsis.

15   Briefly, cH36 treatment attenuated fibrinogen depletion and TAT complex formation, consistent with inhibition of TF-dependent activation of coagulation. In sepsis controls, fibrinogen decreased to approximately 50% of initial values, but in animals treated with cH36 mean fibrinogen levels did not drop below baseline values (Figure 10A, p<0.01 versus sepsis controls). PT increased in sepsis controls during
20   sepsis due to a progressive coagulopathy, and also increased in treated animals due to pharmacologic effect of the drug infusion. PT and fibrinogen values in the three cH36-Fab treated animals are also shown for comparison. The decreased values in the cH36-Fab compared to whole antibody treated animals suggest that the Fab fragment has a lower affinity for TF (Figure 10A,B). PTT increased in both groups
25   and was not significantly different. TAT complexes increased after infusion of live bacteria in both groups, peaking at 14 h and then decreasing. Peak TAT value was lower and levels decreased more rapidly in animals treated with cH36 (Figure 10D, p<0.01). The difference in TAT complex formation was not due to differences in ATIII levels, as ATIII decreased similarly in the two groups, to 35-40% of initial
30   values by the end of the experiment.

E. Results: Treatment with Sunol-cH36 attenuates sepsis-induced acute lung injury

cH36 decreased ALI in baboons with established *E. coli* sepsis, attenuating sepsis-induced abnormalities in gas exchange, pulmonary hypertension, and loss of

5   pulmonary system compliance. These physiologic data are shown in Figures 8A-C. Alveolar arterial oxygen gradient (AaDO$_2$, mmHg) increased in both groups after infusion of killed bacteria and progressively worsened in the sepsis control group after the onset of live bacterial sepsis at t = 12 h. Compared to septic control animals, treatment with cH36 prevented progressive deterioration in gas exchange during

10 sepsis (p = 0.001, Figure 8A). One animal in the sepsis control group required supplemental oxygen after the onset of live bacterial sepsis for progressive hypoxemia. One animal in the cH36 treated group also required oxygen, but only from 18-22 hours, during which oxygenation gradually improved and supplemental O$_2$ was weaned back to room air. At the end of the experiment the AaDO$_2$ in that

15 animal had recovered to initial values measured prior to infusion of heat-killed or live bacteria. Sepsis-induced increase in mean pulmonary artery pressure (PAM, mmHg) was attenuated by cH36 (p < 0.0001 vs. untreated sepsis controls, Fig 8B) but there was no difference in pulmonary vascular resistance, suggesting that this was due to effect on cardiac output in the treated animals. cH36 also prevented the decrease in

20 pulmonary system compliance (Cst in mL/cm H$_2$O) seen in sepsis control animals (p < 0.01, Fig 8C). The PaCO$_2$ was controlled within the normal range, between 35-45 mmHg in both groups, but was slightly higher in sepsis controls (p=0.03) despite 20% higher minute ventilation (V$_E$, l/min, p=0.015), suggesting cH36 attenuated sepsis-induced increases in dead space (Table 7).

25

At post-mortem, the lungs from sepsis control animals were dense and hemorrhagic. The gross appearance of the lungs from animals treated with cH36 was improved and in some animals appeared the same as lungs from normal uninjured baboons. Lung wet/dry weights were not significantly different in the two groups,

30 6.32 ± 0.66 in septic controls compared to 5.57 ± 0.34 in cH36 treated animals (p = NS, normal reference range is 4.6-5.0). BAL protein and LDH were also not significantly different between the two groups. BAL protein was 1.0 ± 0.3 in septic

controls compared to 1.0± 0.4 in cH36 treated animals, and LDH was 23.9 ± 10.6 in septic controls compared to 10.6 ± 3 in cH36 treated animals.   Neutrophil accumulation, as measured by myeloperoxidase (MPO) activity (OD/min/gm wet wt), was decreased over 40% in cH36 treated animals (p=0.07).

5

Lung histology showed protection in septic animals treated with cH36. The lungs of sepsis control animals had thickened alveolar septae, patchy alveolar edema and hemorrhage, and intra-alveolar inflammatory cell infiltration with macrophages and PMNs.   Lungs of treated animals had improved alveolar septal architecture,

10   decreased alveolar PMN infiltration, less alveolar edema, and no alveolar hemorrhage.

EXAMPLE 5: Treatment with cH36 improves renal function and reduces organ injury in sepsis

15

Materials and methods used to perform the present Example have been desribed previously. See eg., Example 4.

Treatment with cH36 improved renal function in sepsis. Urine output was

20   significantly higher after infusion of live *E. coli* in animals treated with cH36 compared to untreated controls (p < 0.001).   This was not due to differences in resuscitation because fluid balance and systemic hemodynamics were similar in the two groups. Blood pH and serum [HCO3⁻] were lower in untreated animals (both p < 0.0001), and values were consistent with mixed metabolic and respiratory acidosis in

25   sepsis controls. Serum creatinine was not different in the two groups at the end of the experiments, and there was variability in the treated group due to one animal that was not protected.

See Figures 13A-C (showing mean urine output (13A), mean blood pH (13B), and serum bicarbonate levels (13C) with control and cH36 antibodies.

30   Kidneys from untreated animals were swollen and hemorrhagic at post mortem but appeared more normal in cH36 treated animals. H&E stained sections of the

kidneys of untreated animals had patchy to extensive areas of acute tubular necrosis (ATN) and glomerular damage. The kidneys of treated animals, except for a few small foci of ATN, showed normal renal architecture. MPO values were significantly decreased in kidneys from treated animals (p=0.01).

5   Other organ injury was also improved in the cH36 treated animals. Adrenals from untreated animals were swollen and hemorrhagic and small bowel was grossly edematous. In contrast, adrenals and small bowel appeared almost normal in animals treated with cH36. Small bowel wet/dry weights were decreased in septic animals treated with cH36 (6.46 ± 0.62 in Sunol-cH36 treated vs. 9.70 ± 1.05 in untreated

10   sepsis control animals, p = 0.01). Histology confirmed improvement in small bowel edema. Adrenals were also protected from sepsis, with decrease in congestion and hemorrhage, and areas of cellular damage were markedly diminished. In addition to the decreased neutrophil content in the lung and kidney, cH36 treatment significantly decreased PMN content in the liver (p=0.05,), and histology showed decreased injury

15   to hepatocytes.

EXAMPLE 6: cH36 treatment attenuated sepsis-induced anemia

20   Materials and methods used to perform the present Example have been explained above. See eg., Example 4.

     Both groups of animals developed neutropenia, thrombocytopenia and anemia after infusion of live *E. coli* (see Table 8, below). Hemoglobin (Hgb) decreased in

25   both groups but was significantly higher in septic animals treated with cH36 (8.1 ± 0.7 versus 10.8 ± 0.8 g/dL at 48 hours, p < 0.0001). Although platelets declined more rapidly in untreated animals (p<0.0001), the clinical significance of this difference is not clear. All animals developed progressive thrombocytopenia after the infusion of live *E. coli* and mean platelet counts were approximately 30,000 or less in both

30   groups at the end of the experiment. WBC reached a nadir of approximately 1,000-1,500 (x $10^3/\mu L$) in both groups two hours after the infusion (t = 14 h) and

progressively increased to baseline levels by the end of the experiment (12,680 ±

2,012 in treated vs. 10,500 ± 1,336 in untreated animals, p = 0.07). Two sepsis

control animals developed self-limited hematuria. Most animals in both groups had

some blood tinged secretions associated with suctioning at some point in the study,

5   but there was no clinical evidence of significant hemorrhage (i.e. hematuria,

hemoptysis, or bleeding from intravenous or arterial catheter sites) in the cH36

treated animals and no severe or life-threatening bleeding complications occurred in

either group.

Table 8

10

Time (h)		0	12	18	24	36	48	p value
Hgb (g/dL)								
	Sepsis	11.2 ± 0.3	10.6 ± 0.3	10.4 ± 0.5	10.4 ± 0.8	8.7 ± 0.8	8.1 ± 0.7	
	cH36	12.1 ± 0.5	11.8 ± 0.4	12.2 ± 0.5	12.4 ± 0.6	10.9 ± 0.8	10.8 ± 0.8	<0.0001
	cH36 Fab	11.7 ± 0.3	11.5 ± 0.5	12.5 ± 0.8	11.4 ± 0.3	11.3 ± 0.4	9.6 ± 0.1	
Platelets								
	Sepsis	194 ± 15	126 ± 12	59 ± 7	33 ± 5	24 ± 5	26 ± 9	
	-cH36	206 ± 15	167 ± 16	110 ± 13	64 ± 12	40 ± 4	30 ± 4	<0.0001
	cH36 Fab	197 ± 8	146 ± 4	87 ± 10	31 ± 5	21 ± 4	25	
HR (beats/min)								
	Sepsis	95 ± 6	116 ± 10	125 ± 9	129 ± 9	125 ± 5	127 ± 16	
	cH36	84 ± 3	101 ± 4	135 ± 13	123 ± 11	105 ± 12	99 ± 9	<0.01
	cH36 Fab	75 ± 7	89 ± 9	107 ± 14	109 ± 9	98 ± 15	98 ± 9	
MAP (mmHg)								
	Sepsis	111 ± 2	104 ± 2	99 ± 9	102 ± 7	79 ± 10	78 ± 13	
	cH36	102 ± 3	93 ± 3	97 ± 5	92 ± 6	78 ± 9	86 ± 5	NS
	cH36 Fab	108 ± 4	85 ± 4	89 ± 9	78 ± 8	89 ± 4	63 ± 4	
CO/kg								
	Sepsis	0.16 ± 0.01	0.20 ± 0.02	0.23 ± 0.04	0.22 ± 0.03	0.22 ± 0.04	0.23 ± 0.02	
	cH36	0.15 ± 0.01	0.18 ± 0.01	0.16 ± 0.02	0.16 ± 0.02	0.15 ± 0.02	0.18 ± 0.01	<0.0001
	cH36 Fab	0.12 ± 0.01	0.14 ± 0.01	0.12 ± 0.01	0.15 ± 0.01	0.14 ± 0.01	0.14 ± 0.02	
D_{O2}/kg								
	Sepsis	23.2 ± 2.2	28.1 ± 3.1	28.6 ± 4.1	26.2 ± 2.0	22.7 ± 24.3	20.1 ± 1.2	
	cH36	23.8 ± 1.8	28.0 ± 1.0	23.8 ± 2.4	24.9 ± 3.5	23.1 ± 2.6	24.6 ± 2.1	NS
	cH36 Fab	18.1 ± 1.6	21.8 ± 2.1	19.5 ± 1.8	20.9 ± 2.7	21.1 ± 1.8	16.4 ± 1.4	
V_{O2}/kg								
	Sepsis	5.4 ± 0.8	6.3 ± 1.4	6.7 ± 0.6	6.8 ± 1.3	5.7 ± 0.6	5.6 ± 0.7	
	cH36	5.6 ± 0.4	6.6 ± 0.2	6.2 ± 0.4	5.6 ± 0.7	6.1 ± 0.6	6.2 ± 0.3	NS
	cH36 Fab	4.0 ± 0.3	4.2 ± 0.2	3.7 ± 0.4	4.6 ± 0.3	3.7 ± 0.2	4.2 ± 0.2	
SVR*kg								
	Sepsis	56602 ± 5459	41539 ± 5049	35290 ± 4941	37788 ± 5675	30713 ± 9152	26161 ± 5750	
	cH36	50833 ± 3782	37936 ± 895	49953 ± 8998	46811 ± 6290	37432 ± 3612	36058 ± 4362	***
	cH36 Fab	69095 ± 2475	43890 ± 5700	52763 ± 7023	39545 ± 7126	46570 ± 5101	32243 ± 8576	
PCWP								
	Sepsis	10 ± 1	11 ± 1	10 ± 1	11 ± 1	12 ± 1	11 ± 1	
	cH36	10 ± 0	10 ± 0	9 ± 1	9 ± 1	11 ± 2	9 ± 1	NS
	cH36 Fab	12 ± 0	14 ± 1	10 ± 1	10 ± 1	11 ± 1	12 ± 2	
V_E								
	Sepsis	3.5 ± 0.3	3.5 ± 0.2	3.8 ± 0.2	4.2 ± 0.2	5.0 ± 0.5	5.1 ± 0.4	
	cH36	3.7 ± 0.1	3.9 ± 0.2	4.0 ± 0.2	4.3 ± 0.2	4.4 ± 0.3	4.3 ± 0.2	=0.015

	cH36 Fab	4.3 ± 0.2	4.4 ± 0.2	4.5 ± 0.1	5.0 ± 0.4	6.4 ± 0.8	6.2 ± 0.9
cH36 (ng/mL)			15 hr				
	cH36	0	49.3 ± 5.5	51.8 ± 3.3	60.2 ± 6.0	53.0 ± 5.6	58.0 ± 8.3
	cH36 Fab	0	±	±	±	±	±

Clinical and histological evaluations are performed to confirm that anti-tissue factor injections inhibited the development of rheumatoid arthritis in these mice.

Referring to the foregoing Examples and discussion, it was found that animals treated with cH36 had a less hyperdynamic systemic response to sepsis. Most systemic hemodynamic measurements, including mean arterial pressure (MAP), PCWP, systemic vascular resistance*kg (SVR*kg), VO_2, and DO_2, were not altered by treatment with cH36 (Table 8). Hypotension responded to IV fluids and dopamine infusion in both groups. Nine of the 12 animals survived until the scheduled termination point of the protocol. Overall, septic animals treated with cH36 were less hyperdynamic, without further increases in cardiac output (CO/kg) after the onset of live bacterial sepsis, and had less tachycardia and higher systemic vascular resistance*kg (SVR*kg) at the end of the experiment (Table 7, for instance). In some instances, treated animals needed dopamine and fluid support as did the untreated controls and MAP and SVR were not detectably different between the two groups. Survival is not intended for use as an endpoint as all animals were sacrificed at the 48 hour time point. Three septic animals were treated with cH36-Fab to assess for differences between whole antibody and Fab fragment. As expected, the whole antibody was often more effective then the Fab fragment.

EXAMPLE 7: Impact of cH36 on pro-inflammatory cytokine levels

Cytokine levels were measured in serum and BAL fluid along lines already described above (eg., Example 5). In the circulation, cH36 treatment attenuated IL-8 ($p<0.01$, Fig. 12) but had no detectable effect on IL-1β, or TNFR-1. In BAL fluid, cH36 attenuated elevations in IL-6, IL-8 and TNFR-1. BAL cytokine levels are shown in Table 9 below. We also measured soluble thrombomodulin (sTM) and found no differences in treated vs. untreated animals in serum or BAL. The data

show that inhibiting coagulation using Sunol-cH36 to block the FX binding site on TF-FVIIa complex attenuates acute lung injury at least in part through effects on proinflammatory cytokine levels in the alveolar compartment. This could be an effect on local cytokine production and/or leakage of proteins from the circulation across the alveolar epithelium.

Table 9. BAL cytokine levels

	Sepsis control	Sunol-cH36	p value	cH36–Fab
IL-6 (pg/mL)	600 ± 269	506 ± 522	0.05	1159 ± 435
IL-8 (pg/mL)	1081 ± 448	224 ± 176	0.037	1478 ± 755
IL-1β (pg/mL)	6.9 ± 1.5	7.9 ± 3.1	NS	8.5 ± 1.8
TNFR1 (pg/mL)	294 ± 126	107 ± 31	0.09	167 ± 93
sTM (ng/mL)	1.67 ± 0.54	0.9 ± 0.11	NS	2.17 ± 0.72

Certain results from Examples 4-7 can be summarized as follows:

Most systemic hemodynamic measurements, including mean arterial pressure (MAP), oxygen consumption (VO2/kg), and oxygen delivery (DO2/kg), were not altered by treatment with cH36 (Table 8). Mean pulmonary capillary wedge pressure (PCWP) was slightly higher in sepsis control animals (p<0.01) but both groups were within the set parameters of the study. Systemic vascular resistance*kg (SVR*kg) was slightly higher in treated animals (p< 0.05, Table 3). Hypotension responded to IV fluids and dopamine infusion in both groups. Nine of the 12 animals survived until the scheduled termination point of the protocol. Two sepsis control animals died prior to scheduled termination from ALI, with refractory hypoxemia and respiratory acidosis, one at 30 hours and one at 38 hours. One animal in the H36 group was not protected and died at 36 hours of refractory hypotension and metabolic acidosis. In that animal, lack of protection correlated with lower drug levels. Overall, septic animals treated with cH36 were less hyperdynamic, without further increases in cardiac output (CO/kg) after the onset of live bacterial sepsis, and had less tachycardia and higher systemic vascular resistance per kg (SVR*kg) at the end of the experiment (Table 7).

EXAMPLE 8: Treatment of Baboons with cH36-Fab (Fab fragment)

Three septic animals were treated with cH36-Fab look for any differences
between use of whole antibody and Fab fragment. Treatment protocols generally
followed procedures already discussed above. Although the group was too small for
detailed statistical analyses, the data suggested that the Fab fragment had effect in
attenuating sepsis-induced activation of coagulation, with increased TAT values and
depletion of fibrinogen similar to septic controls. However, that effect was less
pronounced then results achieved with whole antibody. Correspondingly, there was
less consistent improvement in gas exchange (AaDO2), pulmonary hypertension
(PAM), and lung compliance (Cst) than in animals treated with whole cH36 antibody.
Biochemically, lung MPO values were similar to septic controls. Without wishing to
be bound to theory, the difference in effect between cH36 and its Fab fragment may
be due to the lower affinity of the Fab fragment for TF in the animal model.

EXAMPLE 9: Anti-Tissue Factor Inhibition of Collagen-Induced Arthritis in
Transgenic Mice Expressing Human Tissue Factor

Collagen-induced arthritis (CIA) is an established experimental model of
rheumatoid arthritis which is induced in susceptible strains of mice following
immunization with type II collagen. In addition to the immune mediated mechanism
in the pathogenesis of rheumatoid arthritis, tissue factor initiated activation of the
coagulation cascade has also been implicated in the progression of the disease. Fibrin
deposition in the affected joints resulting from the activation of coagulation is
believed to contribute to synovial thickening and joint inflammation. To determine
whether treatment with anti-tissue factor antibodies will prevent development of
rheumatoid arthritis mice will be injected with cH36.

To induce CIA 7-12 week old mice are injected intradermally at the base of the tail with 100μg of type II collagen emulsified in Complete Freund's Adjuvant and given a boost injection with 100 μg of type II collagen emulsified in Incomplete Freund's Adjuvant at day 21. Immediately prior to the boost injection mice are given

5   0.3 mg anti-tissue factor antibody by IV injection (the control group are injected with PBS). Anti-tissue factor antibody injections (0.3 mg) are subsequently given weekly for the duration of the study (the control group are injected with PBS).

Animals are assessed for redness and swelling of the limbs and a clinical

10   score is allocated three times per week. The clinical severity is scored as follows: 1 point for each swollen digit except the thumb (maximum 4), 1 Point for the tarsal or carpal joint, and one point for the metatarsal or metacarpal joint with a maximum score of 6 for a hindpaw and 5 for a forepaw. Each paw is graded individually, the cumulative clinical arthritic score per mouse can reach a maximum of 22 points.

15

The present provisional application has information relating to published U.S. patent application no. 20030190705 which application is related to U.S Application No. 09/990,586 as filed on November 21, 2001, which application claims priority to U.S. Provisional Application USSN 60/343,306 as filed on October 29, 2001. The

20   U.S Application No. 09/990,586 is related to U.S. Application No. 09/293,854 (now U.S. Pat. No. 6,555,319) which application is a divisional of U.S. Application No. 08/814,806 (now U.S. Pat. No. 5,986,065) and the U.S. Application No. 10/230,880 claims priority to U.S Application No. 09/990,586. The disclosures of the U.S. Application Nos. 10/230,880, 09/990,586, 60/343,306 and U.S. Pat. Nos. 5,986,065

25   and 6,555,319 are each incorporated by reference. Also incorporated by reference is the disclosure of published U.S. patent application no. 20030190705.

The present provisional application is further related to U.S. provisional application Serial No. 60/480,254 as filed on June 19, 2003, the disclosure of which

30   is incorporated by reference.

The invention has been described in detail with reference to preferred embodiments thereof. However, it will be appreciated that those skilled in the art, upon consideration of the disclosure, may make modification and improvements within the spirit and scope of the invention. All references disclosed herein are incorporated herein by reference.

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What is claimed is:

1.   A method for preventing or treating a sepsis or inflammatory disease in a
mammal, the method comprising administering to the mammal a therapeutically
5   effective amount of at least one humanized antibody, chimeric antibody, or fragment
thereof that binds specifically to tissue factor (TF) to form a complex, wherein factor
X or factor IX binding to the complex is inhibited and the administration is sufficient
to prevent or treat the sepsis in the mammal.

10   2.   The method of claim 1, wherein the humanized antibody, chimeric antibody
or the fragment exhibits at least one of: 1) a dissociation constant (K_d) for the TF of
less than about 0.5 nM; or 2) an affinity constant (K_a) for the TF of less than about 10
x 10^{10} M^{-1}.

15   3.   The method of claims 1-2, wherein the humanized antibody, chimeric
antibody or fragment thereof is further characterized by having a binding specificity
for the TF about equal or greater than the antibody obtained from cell line H36.D2.B7
deposited under ATCC Accession No. HB-12255.

20   4.   The method of claims 1-3, wherein the humanized antibody, chimeric
antibody or fragment thereof is further characterized in that factor X or factor IX
activation by the TF-factor VIIa complex is blocked.

5.   The method of claims 1-4, wherein administration of the humanized antibody,
25   chimeric antibody or fragment to the mammal increases survival time by at least
about 2-fold as determined by a standard *in vivo* septic shock assay.

6.   The method of claims 1-5, wherein administration of the humanized antibody,
chimeric antibody or fragment to the mammal attenuates at least one of inflammatory
30   cytokine (interleukin-6 (IL-6) and interleukin-8 (IL-8), interleukin-1beta (IL-1β),

tumor necrosis factor-alpha (TNFα) or tumor necrosis factor receptor (TNFR)) levels in the mammal after at least about 5 hours.

7.   The method of claims 1-6, wherein about 5 minutes after administration of the
5 humanized antibody, chimeric antibody or fragment, the mammal exhibits a blood clotting time of between from about 30 to about 350 seconds as determined by a standard prothrombin time assay.

8.   The method of claims 1-7, wherein the amount of the administered humanized
10 antibody, chimeric antibody, or fragment is sufficient to inhibit platelet deposition by at least about 50% as determined by a standard platelet deposition assay.

9.   The method of claims 1-8, wherein the humanized antibody has an IgG1 or IgG4 isotype.
15

10.   The method of claims 1-9, wherein the human TF binding fragment is Fab, Fab', or F(ab)$_2$.

11.   The method of claims 1-10, wherein the humanized antibody is a monoclonal
20 antibody.

12.   The method of claims 1-10, wherein the humanized antibody or fragment thereof is a single-chain.

25 13.   The method of claims 1-28, wherein the mammal is a primate.

14.   The method of claim 13, wherein the primate is a human patient.

15.   The method of claims 1-14, wherein the sepsis is associated with at least one
30 of disseminated intravascular coagulation (DIC), fibrin deposition, thrombosis, and lung injury.

16.   The method of claims 1-14, wherein the inflammatory disease is associated with at least one of arthritis, preferably rheumatoid arthritis, glomerulonephritis, multiple sclerosis, psoriasis, Sjogren's syndrome and inflammatory bowel disease.

17.   The method of claims 1-28, wherein the amount of the humanized antibody, chimeric antibody or fragment administered to the mammal is between about 0.01 to about 25 (mg/kg).

18.   A kit for performing the method of claims 1-16, wherein the kit includes at least one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to human TF to form a complex, wherein factor X or factor IX binding to the complex is inhibited.

19.   The kit of claim 17, wherein the humanized antibody, chimeric antibody, or fragment thereof is provided in a pharmaceutically acceptable vehicle.

20.   The kit of claims 17-18, wherein the humanized antibody, chimeric antibody, or fragment thereof is lyophilized and the kit further includes a pharmaceutically acceptable vehicle for dissolving the humanized antibody, chimeric antibody or fragment.

21.   A method for reducing an inflammatory cytokine production in a mammal, the method comprising administering to the mammal a therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment thereof that binds specifically to TF to form a complex, wherein factor X or factor IX binding to the complex is inhibited and the administration is sufficient to reduce the inflammatory cytokine production in the mammal.

22.   The method of claim 21, wherein the inflammatory cytokine is at least one of inflammatory cytokine (interleukin-6 (IL-6) and interleukin-8 (IL-8), interleukin-

1beta (IL-1β), tumor necrosis factor-alpha (TNFα) or tumor necrosis factor receptor (TNFR)).

23.   The method of claims 21-22, wherein the administered antibody, chimeric
5   antibody or fragment there of is encompassed by any one of claims 2-12.

22.   A method for preventing or treating a sepsis-related condition in a mammal, the method comprising administering to the mammal a therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment thereof
10   that binds specifically to tissue factor (TF) to form a complex, wherein factor X or factor IX binding to the complex is inhibited and the administration is sufficient to prevent or treat the condition in the mammal.

23.   The method of claim 22, wherein the sepsis-related condition is one or more
15   of disseminated intravascular coagulation (DIC), fibrin deposition, thrombosis,lung injury, or sepsis-associated renal disorder .

24.   The method of claim 23, wherein the lung injury is acute lung injury (ALI), or acute respiratory distress syndrome (ARDS).
20
25.   The method of claim 23, wherein the sepsis-associated renal disorder is acute tubular necrosis (ACN).

26.   The method of claims 22-25, wherein the administered antibody, chimeric
25   antibody or fragment there of is encompassed by any one of claims 2-12.

27.   A method for preventing or treating sepsis-induced anemia in a mammal, the method comprising administering to the mammal a therapeutically effective amount of at least one humanized antibody, chimeric antibody, or fragment thereof that binds
30   specifically to tissue factor (TF) to form a complex, wherein factor X or factor IX

binding to the complex is inhibited and the administration is sufficient to prevent or treat the condition in the mammal.

28.   The method of claim 27, wherein the administered antibody, chimeric
5   antibody or fragment there of is encompassed by any one of claims 2-12.

H36.D2.B7 Anti-Tissue Factor Light Chain Variable Domain

```
 5   GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTGTGGGAGAAAGTGTCACCATCACATGC
      D   I   Q   M   T   Q   S   P   A   S   Q   S   A   S   L   G   E   S   V   T   I   T   C

     CTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCAGGGAAATCTCCTCAGCTC
      L   A   S   Q   T   I   D   T   W   L   A   W   Y   Q   Q   K   P   G   K   S   P   Q   L

     CTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCAAGGTTCAGTGGCAGTGGATCTGGCACA
      L   I   Y   A   A   T   N   L   A   D   G   V   P   S   R   F   S   G   S   G   S   G   T

10   AAATTTTCTTTCAAGATCAGCAGCCTACAGCCTGAAGATTTTGTAAATTATTACTGTCAACAAGTTTAC
      K   F   S   F   K   I   S   S   L   Q   A   E   D   F   V   N   Y   Y   C   Q   Q   V   Y

     AGTTCTCCATTCACGTTCGGTGCTGGGACCAAGCTGGAGCTGAAA
      S   S   P   F   T   F   G   A   G   T   K   L   E   L   K
```

FIG. 1A

FIG. 1B

H36.D3.B7 Anti-Tissue Factor Heavy Chain Variable Domain

GAGATCCAGCTGCAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGCAGGTATCCTGCAAG
E　I　Q　L　Q　Q　S　G　P　E　L　V　K　P　G　A　S　V　Q　V　S　C　K

ACTTCTGGTTACTCATTCACTGACTACAACGTGTACTGGGTGAGGCAGAGCCATGGAAAGAGCCTTGAG
T　S　G　Y　S　F　T　D　Y　N　V　Y　W　V　R　Q　S　H　G　K　S　L　E

20

TGGATTGGATATATTGATCCTTACAATGGTATTACTATCTACGACCAGAACTTCAAGGGCAAGGCCACA
W　I　G　Y　I　D　P　Y　N　G　I　T　I　Y　D　Q　N　F　K　G　K　A　T

TTGACTGTTGACAAGTCTTCCACCAGCTTCATGCATCTCAACAGCCTGACATCTGACGACTCTGCA
L　T　V　D　K　S　S　T　A　F　M　H　L　N　S　L　T　S　D　D　S　A

GTTTATTTCTGTGCAAGAGATGTGACTACGGCCCTTGACTTCTGGGGCCAAGGCACCACTCTCACAGTC
V　Y　F　C　A　R　D　V　T　T　A　L　D　F　W　G　Q　G　T　T　L　T　V

25

TCCTCA
S　S

CDR REGIONS UNDERLINED (single underline for nucleic acid sequence and
double underline for amino acid sequence)

FIG. 2

Notes: 1. Amino acid sequence in one letter code.
       2. Immediately following the last residue of the framework 4(FR4) variable domain is the first residue of the constant domain for hOAT or hFAT.

```
FR1 (23 AA)              FR2 (15 AA)      FR3 (32 AA)                         FR4 (10 AA) Names
1            10      20  35               49 57 60        70        80  88 98            88 98    107
 5 DIQMTQSPASQSASLGESVTITC WYQQKPGKSPQLIY  GVESRFSGSGSGTKFSFKISSLQAEDFVNYYC  FGAGTKLELK  cH36-LC
   DIQMTQSPASQSASLGESVTITC WYQQKPGKSPQLIY  GVPSRFSGSGSGTKFSFKISSLQAEDFVNYYC  FGAGTKLEIK  LC-03
   DIQMTQSPASQSASLGESVTITC WYLQKPGKSPQLIY  GVPS FSGSGSGTKFSFKISSLQAEDFVNYYC  FGAGTKLEIK  LC-04
   DIQMTQSPASLSASVGDRVTITC WYLQKPGKSPQLIY  GVPSRFSGSGSGTKFSFKISSLQAEDFVNYYC  FGQGTKLEIK  LC-05
   DIQMTQSPASQSASLGESVTITC WYLQKPGKSPQLIY  GVPSRFSGSGSGTKFSFKISSLQAEDFVNYYC  FGQGTKLEIK  LC-06
10 DIQMTQSPASQSASLGESVTITC WYLQKPGKSPQLIY  GVPSRFSGSGSGTDFSFTISSLQPEDFVNYYC  FGQGTKLEIK  LC-07
   DIQMTQSPASQSASLGESVTITC WYLQKPGKSPQLIY  GVPSRFSGSGSGTDFSFTISSLQPEDFATYYC  FGQGTKLEIK  LC-08
   DIQMTQSPASLSASVGDRVTITC WYLQKPGKSPQLIY  GVPSRFSGSGSGTDFSFTISSLQPEDFATYYC  FGQGTKLEIK  LC-09
   DIQMTQSPASLSASVGDRVTITC WYLQKPGKSPQLIY  GVPSRFSGSGSGTDFSFTISSLQPEDFANYYC  FGQGTKLEIK  LC-10
   DIQMTQSPASLSASVGDRVTITC WYLQKPGKSPQLIY  GVPSRFSGSGSGTDFSFTISSLQPEDFANYYC  FGQGTKLEIK  LC-11
15 DIQMTQSPASLSASVGDRVTITC WYLQKPGQSPQLIY  GVPSRFSGSGSGTKFSFTISSLQPEDFANYYC  FGQGTKLEIK  LC-12
```

FIG. 3A

Light Chain CDR Sequences of cH36

CDR1 (11 AA)
24   34
L A S Q T I D T W L A

FIG. 3B

CDR2 (7 AA)
50   56
A A T N L A D

FIG. 3C

CDR3 (9 AA)
89   97
Q Q V Y S S P F T

FIG. 3D

Exept for HC-08, all others HC mutants and cH36 contain F at position 64 in CDR2.
KC-08 has the mutation F64 to L (change from F to L at position 64)

FR1 (30 AA)	FR2 (14 AA)	FR3 (32 AA)	FR4 (11 AA)	Names
1	20 30 36	49 67 75 85 95	107 117	
EIQLQQSGPELVKPGASVQVSCKTSGYSFT	WVRQSHGKSLEWIG	KATLTVDKSSTTAFMHLNSLTSDDSAVYFCAR	WGQGTTLTVSS	CH36-HC
QIQLQQSGPELVKPGASVQVSCKTSGYSFT	WVRQSHGKSLEWIG	KATLTVDKSSTTAFMHLNSLTSDDSAVYFCAR	WGQGTTVTVSS	HC-01
QIQLQQSGPELVKPGASVQVSCKTSGYSFT	WVRQSPGKGLEWIG	KATLTVDKSSTTAFMHLNSLTSDDSAVYFCAR	WGQGTTVTVSS	HC-02
QIQLQQSGPELVKPGASVQVSCKTSGYSFT	WVRQSPGKGLEWIG	KATLTVDKSSTTAFMHLNSLRSEDTAVYFCAR	WGQGTTVTVSS	HC-03
QIQLQQSGPELVKPGASVQVSCKTSGYSFT	WVRQSPGKGLEWIG	KATLTVDKSSTTAFMELSSLRSEDTAVYFCAR	WGQGTTVTVSS	HC-04
QIQLQQSGPELVKPGASVQVSCKTSGYSFT	WVRQSPGKGLEWIG	KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR	WGQGTTVTVSS	HC-05
QMQLQQSGGELVKPGASVQVSCKTSGYSFT	WVRQSPGKGLEWIG	KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR	WGQGTTVTVSS	HC-06
QIQLVQSGGELVKPGASVRVSCKASGYSFT	WVRQSPGKGLEWIG	KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR	WGQGTTVTVSS	HC-07
QIQLVQSGGEVKKPGASVRVSCKASGYSFT	WVRQSPGKGLEWIG	KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR	WGQGTTVTVSS	HC-08
QIQLVQSGGEVKKPGASVRVSCKASGYSFT	WVRQSPGKGLEWIG	KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR	WGQGTTVTVSS	HC-08R1
QIQLVQSGPEVKKPGASVRVSCKASGYSFT	WVRQSPGKGLEWIG	KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR	WGQGTTVTVSS	HC-11
QIQLVQSGPELKKPGASVRVSCKASGYSFT	WVRQSPGKGLEWIG	KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR	WGQGTTVTVSS	HC-12
QIQLVQSGPEVKKPGASVRVSCKASGYSFT	WVRQSPGKGLEWIG	KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR	WGQGTTVTVSS	HC-09
QIQLVQSGPEVVKPGASVRVSCKASGYSFT	WVRQSPGKGLEWIG	KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR	WGQGTTVTVSS	HC-10

FIG. 4A

Heavy Chain CDR Sequences

CDR1 (5aa)	
31 35	
D Y N V Y	
D Y N V Y	

FIG. 4B

CDR2 (17 AA)	
50 66	
Y I D P Y N G I T I Y D Q N F K G	
Y I D P Y N G I T I Y D Q N L K G	

FIG. 4C

CDR3 (8AA)		Names
99 106		
D V T T A L D F		cH36
D V T T A L D F		HC-08

FIG. 4D

Sequence of human kappa Light Chain Constant Domain:

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKH
KVYACEVTHQGLSSPVTKSFNRGEC

FIG. 5A

Sequence of human IgG1 Heavy Chain Constant Domain:

EFASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL
VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Notes: 1. Amino acid sequence in one letter code.
2. Immediatly following the last residue of the framework 4 (FR4) variable domain is the first residue of the constant domain for hOAT or hFAT.
3. LC constant are the same for hOAT and hFAT.

FIG. 5B

Sequence of human kappa Light Chain Constant Domain:

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEK

HKVYACEVTHQGLSSPVTKSFNRGEC

FIG. 6A

Sequence of human IgG4 Heavy Chain Constant Domain:

EFASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTY

TCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGV

EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSL

TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

Notes: 1. Amino acid sequence in one letter code.
       2. Immediately following the last residue of the framework 4 (FR4)
          variable domain is the first residue of the constant domain for
          hOAT or hFAT.
       3. LC constant domain is the same for hOAT and hFAT.

FIG. 6B

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FIG. 7A

FIG. 7B

FIG. 7C

FIG. 7D

FIG. 8A

FIG. 8B

FIG. 8C

FIG. 9A

FIG. 9B

FIG. 10A

PT

FIG. 10B

PTT

FIG. 10C

FIG. 10D

FIG. 11A

FIG. 11B

FIG. 12

Mean Urine Output

FIG. 13A

Mean Blood pH

FIG. 13B

SEQUENCE LISTING

(1) GENERAL INFORMATION

5

(i) APPLICANT:

(ii) TITLE OF THE INVENTION:

10   (iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:
     (A) ADDRESSEE:
     (B) STREET:
15   (C) CITY:
     (D) STATE:
     (E) COUNTRY:
     (F) ZIP:

20   (v) COMPUTER READABLE FORM:
     (A) MEDIUM TYPE: Diskette
     (B) COMPUTER: IBM Compatible
     (C) OPERATING SYSTEM: DOS
     (D) SOFTWARE: FastSEQ Version 1.5
25
     (vi) CURRENT APPLICATION DATA:
     (A) APPLICATION NUMBER:
     (B) FILING DATE:
     (C) CLASSIFICATION:
30
     (vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER:
     (B) FILING DATE:

35   (viii) ATTORNEY/AGENT INFORMATION:
     (A) NAME:
     (B) REGISTRATION NUMBER:
     (C) REFERENCE/DOCKET NUMBER:

40   (ix) TELECOMMUNICATION INFORMATION:
     (A) TELEPHONE:
     (B) TELEFAX:
     (C) TELEX:

45   (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 321 base pairs
     (B) TYPE: nucleic acid
50   (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
55   (iv) ANTISENSE: NO

        (v) FRAGMENT TYPE:
        (vi) ORIGINAL SOURCE:

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
5   GACATTCAGA TGACCCAGTC TCCTGCCTCC CAGTCTGCAT CTCTGGGAGA AAGTGTCACC
     60
     ATCACATGCC TGGCAAGTCA GACCATTGAT ACATGGTTAG CATGGTATCA GCAGAAACCA
     120
     GGGAAATCTC CTCAGCTCCT GATTTATGCT GCCACCAACT TGGCAGATGG GGTCCCATCA
10   180
     AGGTTCAGTG GCAGTGGATC TGGCACAAAA TTTTCTTTCA AGATCAGCAG CCTACAGGCT
     240
     GAAGATTTTG TAAATTATTA CTGTCAACAA GTTTACAGTT CTCCATTCAC GTTCGGTGCT
     300
15   GGGACCAAGC TGGAGCTGAA A
     321
            (2) INFORMATION FOR SEQ ID NO:2:

        (i) SEQUENCE CHARACTERISTICS:
20   (A) LENGTH: 107 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

25   (ii) MOLECULE TYPE: peptide
        (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
        (v) FRAGMENT TYPE: N-terminal
        (vi) ORIGINAL SOURCE:
30
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

     Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Gln Ser Ala Ser Leu Gly
      1   5   10   15
35   Glu Ser Val Thr Ile Thr Cys Leu Ala Ser Gln Thr Ile Asp Thr Trp
                  20   25   30
     Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Gln Leu Leu Ile
                  35   40   45
     Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
40   50   55   60
     Ser Gly Ser Gly Thr Lys Phe Ser Phe Lys Ile Ser Ser Leu Gln Ala
     65   70   75   80
     Glu Asp Phe Val Asn Tyr Tyr Cys Gln Gln Val Tyr Ser Ser Pro Phe
                      85   90   95
45   Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
                  100   105

            (2) INFORMATION FOR SEQ ID NO:3:

50   (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 351 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
55
        (ii) MOLECULE TYPE: DNA

```
                    (iii) HYPOTHETICAL: NO
                    (iv) ANTISENSE: NO
                    (v) FRAGMENT TYPE:
                    (vi) ORIGINAL SOURCE:
     5
                    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

          GAGATCCAGC TGCAGCAGTC TGGACCTGAG CTGGTGAAGC CTGGGGCTTC AGTGCAGGTA
          60
    10    TCCTGCAAGA CTTCTGGTTA CTCATTCACT GACTACAACG TGTACTGGGT GAGGCAGAGC
          120
          CATGGAAAGA GCCTTGAGTG GATTGGATAT ATTGATCCTT ACAATGGTAT TACTATCTAC
          180
          GACCAGAACT TCAAGGGCAA GGCCACATTG ACTGTTGACA AGTCTTCCAC CACAGCCTTC
    15    240
          ATGCATCTCA ACAGCCTGAC ATCTGACGAC TCTGCAGTTT ATTTCTGTGC AAGAGATGTG
          300
          ACTACGGCCC TTGACTTCTG GGGCCAAGGC ACCACTCTCA CAGTCTCCTC A
          351
    20
                         (2) INFORMATION FOR SEQ ID NO:4:

                    (i) SEQUENCE CHARACTERISTICS:
                         (A) LENGTH: 117 amino acids
    25                   (B) TYPE: amino acid
                         (C) STRANDEDNESS: single
                         (D) TOPOLOGY: linear

                    (ii) MOLECULE TYPE: peptide
    30              (iii) HYPOTHETICAL: NO
                    (iv) ANTISENSE: NO
                    (v) FRAGMENT TYPE: N-terminal
                    (vi) ORIGINAL SOURCE:

    35              (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

          Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
          1               5                   10                  15
          Ser Val Gln Val Ser Cys Lys Thr Xaa Gly Tyr Ser Phe Thr Asp Tyr
    40                  20                  25                  30
          Asn Val Tyr Trp Val Arg Gln Ser His Gly Lys Ser Leu Glu Trp Ile
                  35                  40                  45
          Gly Tyr Ile Asp Pro Tyr Asn Gly Ile Thr Ile Tyr Asp Gln Asn Phe
                  50                  55                  60
    45    Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Phe
          65                  70                  75                  80
          Met His Leu Asn Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys
                          85                  90                  95
          Ala Arg Asp Val Thr Thr Ala Leu Asp Phe Trp Gly Gln Gly Thr Thr
    50                  100                 105                 110
          Leu Thr Val Ser Ser
                  115

                         (2) INFORMATION FOR SEQ ID NO:5:
    55
                    (i) SEQUENCE CHARACTERISTICS:
```

```
                    (A)  LENGTH:  7 amino acids
                    (B)  TYPE: amino acid
                    (C)  STRANDEDNESS:  single
                    (D)  TOPOLOGY:  linear
 5
                  (ii)  MOLECULE TYPE:  peptide
                 (iii)  HYPOTHETICAL:  NO
                  (iv)  ANTISENSE:  NO
                   (v)  FRAGMENT TYPE:  N-terminal
10               (vi)  ORIGINAL SOURCE:

                  (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:5:

     Leu Ala Ser Gln Thr Ile Asp
15   1                5

                (2)  INFORMATION FOR SEQ ID NO:6:

                   (i)  SEQUENCE CHARACTERISTICS:
20                  (A)  LENGTH:  7 amino acids
                    (B)  TYPE:  amino acid
                    (C)  STRANDEDNESS:  single
                    (D)  TOPOLOGY:  linear

25                (ii)  MOLECULE TYPE:  peptide
                 (iii)  HYPOTHETICAL:  NO
                  (iv)  ANTISENSE:  NO
                   (v)  FRAGMENT TYPE:  N-terminal
                  (vi)  ORIGINAL SOURCE:
30                (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:6:

     Ala Ala Thr Asn Leu Ala Asp
      1                5

35              (2)  INFORMATION FOR SEQ ID NO:7:

                   (i)  SEQUENCE CHARACTERISTICS:
                    (A)  LENGTH:  9 amino acids
                    (B)  TYPE:  amino acid
40                  (C)  STRANDEDNESS:  single
                    (D)  TOPOLOGY:  linear

                  (ii)  MOLECULE TYPE:  peptide
                 (iii)  HYPOTHETICAL:  NO
45                (iv)  ANTISENSE:  NO
                   (v)  FRAGMENT TYPE:  N-terminal
                  (vi)  ORIGINAL SOURCE:

                  (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:7:
50
     Gln Gln Val Tyr Ser Ser Pro Phe Thr
      1                5

                (2)  INFORMATION FOR SEQ ID NO:8:
55
                   (i)  SEQUENCE CHARACTERISTICS:
```

```
                    (A) LENGTH: 6 amino acids
                    (B) TYPE: amino acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear
 5
                (ii) MOLECULE TYPE: peptide
                (iii) HYPOTHETICAL: NO
                (iv) ANTISENSE: NO
                (v) FRAGMENT TYPE: N-terminal
10              (vi) ORIGINAL SOURCE:

                (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

    Thr Asp Tyr Asn Val Tyr
15  1               5

               (2) INFORMATION FOR SEQ ID NO:9:

                (i) SEQUENCE CHARACTERISTICS:
20                  (A) LENGTH: 17 amino acids
                    (B) TYPE: amino acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear

25              (ii) MOLECULE TYPE: peptide
                (iii) HYPOTHETICAL: NO
                (iv) ANTISENSE: NO
                (v) FRAGMENT TYPE: N-terminal
                (vi) ORIGINAL SOURCE:
30
                (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

    Tyr Ile Asp Pro Tyr Asn Gly Ile Thr Ile Tyr Asp Gln Asn Phe Lys
    1               5                   10                  15
35  Gly

               (2) INFORMATION FOR SEQ ID NO:10:

                (i) SEQUENCE CHARACTERISTICS:
40                  (A) LENGTH: 8 amino acids
                    (B) TYPE: amino acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear

45              (ii) MOLECULE TYPE: peptide
                (iii) HYPOTHETICAL: NO
                (iv) ANTISENSE: NO
                (v) FRAGMENT TYPE: N-terminal
                (vi) ORIGINAL SOURCE:
50
                (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

    Asp Val Thr Thr Ala Leu Asp Phe
    1               5
55
               (2) INFORMATION FOR SEQ ID NO:11:
```

```
            (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 21 base pairs
               (B) TYPE: nucleic acid
  5            (C) STRANDEDNESS: single
               (D) TOPOLOGY: linear

           (ii) MOLECULE TYPE: DNA
          (iii) HYPOTHETICAL: NO
 10        (iv) ANTISENSE: NO
            (v) FRAGMENT TYPE:
           (vi) ORIGINAL SOURCE:

           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
 15
     CTGGCAAGTC AGACCATTGA T
        21

                (2) INFORMATION FOR SEQ ID NO:12:
 20
            (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 21 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: single
 25            (D) TOPOLOGY: linear

           (ii) MOLECULE TYPE: DNA
          (iii) HYPOTHETICAL: NO
           (iv) ANTISENSE: NO
 30        (v) FRAGMENT TYPE:
           (vi) ORIGINAL SOURCE:

           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

 35  GCTGCCACCA ACTTGGCAGA T
        21

                (2) INFORMATION FOR SEQ ID NO:13:

 40        (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 28 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: single
               (D) TOPOLOGY: linear
 45
           (ii) MOLECULE TYPE: DNA
          (iii) HYPOTHETICAL: NO
           (iv) ANTISENSE: NO
            (v) FRAGMENT TYPE:
 50        (vi) ORIGINAL SOURCE:

           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

     CAACAAGTTT ACAGTTCTCC ATTCACGT
 55     28
```

(2) INFORMATION FOR SEQ ID NO:14:

       (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 18 base pairs
5   (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: DNA
10   (iii) HYPOTHETICAL: NO
      (iv) ANTISENSE: NO
       (v) FRAGMENT TYPE:
      (vi) ORIGINAL SOURCE:

15   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

    ACTGACTACA ACGTGTAC
    18
             (2) INFORMATION FOR SEQ ID NO:15:
20
       (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 51 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
25   (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: DNA
      (iii) HYPOTHETICAL: NO
      (iv) ANTISENSE: NO
30   (v) FRAGMENT TYPE:
      (vi) ORIGINAL SOURCE:

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

35 TATATTGATC CTTACAATGG TATTACTATC TACGACCAGA ACTTCAAGGG C
    51
             (2) INFORMATION FOR SEQ ID NO:16:

40   (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 24 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear
45
      (ii) MOLECULE TYPE: cDNA
      (iii) HYPOTHETICAL: NO
      (iv) ANTISENSE: NO
       (v) FRAGMENT TYPE:
50   (vi) ORIGINAL SOURCE:

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

    GATGTGACTA CGGCCCTTGA CTTC
55 24
             (2) INFORMATION FOR SEQ ID NO:17:

          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 23 base pairs
              (B) TYPE: nucleic acid
 5   (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: DNA
          (iii) HYPOTHETICAL: NO
10   (iv) ANTISENSE: NO
          (v) FRAGMENT TYPE:
          (vi) ORIGINAL SOURCE:

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
15
     GCACCTCCAG ATGTTAACTG CTC
        23

              (2) INFORMATION FOR SEQ ID NO:18:
20
          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 20 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
25   (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: DNA
          (iii) HYPOTHETICAL: NO
          (iv) ANTISENSE: NO
30   (v) FRAGMENT TYPE:
          (vi) ORIGINAL SOURCE:

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
     GAARTAVCCC TTGACCAGGC
35   20

              (2) INFORMATION FOR SEQ ID NO:19:

          (i) SEQUENCE CHARACTERISTICS:
40   (A) LENGTH: 35 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

45   (ii) MOLECULE TYPE: DNA
          (iii) HYPOTHETICAL: NO
          (iv) ANTISENSE: NO
          (v) FRAGMENT TYPE:
          (vi) ORIGINAL SOURCE:
50
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

     GGAGGCGGCG GTTCTGACAT TGTGMTGWCM CARTC
        35
55
              (2) INFORMATION FOR SEQ ID NO:20:

```
            (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 45 base pairs
               (B) TYPE: nucleic acid
  5            (C) STRANDEDNESS: single
               (D) TOPOLOGY: linear

            (ii) MOLECULE TYPE: DNA
            (iii) HYPOTHETICAL: NO
 10         (iv) ANTISENSE: NO
            (v) FRAGMENT TYPE:
            (vi) ORIGINAL SOURCE:

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
 15
      ATTTCAGGCC CAGCCGGCCA TGGCCGARGT YCARCTKCAR CARYC
         45


            (2) INFORMATION FOR SEQ ID NO:21:
 20
            (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 33 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: single
 25            (D) TOPOLOGY: linear

            (ii) MOLECULE TYPE: DNA
            (iii) HYPOTHETICAL: NO
            (iv) ANTISENSE: NO
 30         (v) FRAGMENT TYPE:
            (vi) ORIGINAL SOURCE:

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

 35   CCCGGGCCAC CATGKCCCCW RCTCAGYTYC TKG
         33


            (2) INFORMATION FOR SEQ ID NO:22:

 40         (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 35 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: single
               (D) TOPOLOGY: linear
 45
            (ii) MOLECULE TYPE: DNA
            (iii) HYPOTHETICAL: NO
            (iv) ANTISENSE: NO
            (v) FRAGMENT TYPE:
 50         (vi) ORIGINAL SOURCE:

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

      CCCGGGCCAC CATGGRATGS AGCTGKGTMA TSCTC
 55      35
```

(2) INFORMATION FOR SEQ ID NO:23:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 52 base pairs
5   (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA
10   (iii) HYPOTHETICAL: NO
    (iv) ANTISENSE: NO
    (v) FRAGMENT TYPE:
    (vi) ORIGINAL SOURCE:

15   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATATACTCGC GACAGCTACA GGTGTCCACT CCGAGATCCA GCTGCAGCAG TC
52

20   (2) INFORMATION FOR SEQ ID NO:24:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 31 base pairs
      (B) TYPE: nucleic acid
25   (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA
   (iii) HYPOTHETICAL: NO
30   (iv) ANTISENSE: NO
    (v) FRAGMENT TYPE:
    (vi) ORIGINAL SOURCE:

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
35
GACCTGAATT CTAAGGAGAC TGTGAGAGTG G
31

     (2) INFORMATION FOR SEQ ID NO:25:
40
    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 29 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
45   (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA
   (iii) HYPOTHETICAL: NO
    (iv) ANTISENSE: NO
50   (v) FRAGMENT TYPE:
    (vi) ORIGINAL SOURCE:

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

55 TTAATTGATA TCCAGATGAC CCAGTCTCC
29

(2) INFORMATION FOR SEQ ID NO:26:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 45 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA
    (iii) HYPOTHETICAL: NO
    (iv) ANTISENSE: NO
    (v) FRAGMENT TYPE:
    (vi) ORIGINAL SOURCE:

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TAATCGTTCG AAAAGTGTAC TTACGTTTCA GCTCCAGCTT GGTCC
45

<table>
<tr><td colspan="2">INTERNATIONAL SEARCH REPORT</td><td>International application No.
PCT/US04/17900</td></tr>
</table>

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : A61K 39/40, 39/42, 39/395; G01N 33/53; C12P 21/08; C07K 16/00

US CL : 424/133.1, 134.1, 141.1, 146.1; 435/7.1; 530/387.3, 388.1, 388.26

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 424/133.1, 134.1, 141.1, 146.1; 435/7.1; 530/387.3, 388.1, 388.26

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Continuation Sheet

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 03/029295 A1, 10 April 2003 (see entire document)	1-2, 4-17, 21-28 ---------- 3, 18-20,
Y	US 5,986,065 (Wong et al.) 16 November 1999 (see entire document)	1-28
Y	US 5,223,427 (Edgington et al.) 29 June 1993 (see entire document)	1-28
X/E	US 6,703,494 (Kirchhofer et al.) 9 March 2004 (see entire document)	1-28

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

*	Special categories of cited documents:
"A"	document defining the general state of the art which is not considered to be of particular relevance
"E"	earlier application or patent published on or after the international filing date
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O"	document referring to an oral disclosure, use, exhibition or other means
"P"	document published prior to the international filing date but later than the priority date claimed

"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&"	document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
04 April 2005 (04.04.2005)	**18 MAY 2005**

Name and mailing address of the ISA/US	Authorized officer
Mail Stop PCT, Attn: ISA/US Commissioner for Patents P.O. Box 1450 Alexandria, Virginia 22313-1450	Michael Szperka Telephone No. (571) 272-1600
Facsimile No. (703) 305-3230	

Form PCT/ISA/210 (second sheet) (January 2004)

INTERNATIONAL SEARCH REPORT

Continuation of B. FIELDS SEARCHED Item 3:
MEDLINE, BIOSIS, CAPLUS, EMBASE, SCISEARCH, USPATFULL, USPGPUB, DERWENT WPI
tissue factor, TF, antibody, immunoglobulin, monoclonal, sepsis, kit, ATTC HB-12255